GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen

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                                                                                                                                                                                         Query
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arr	10	22	386	7.	w
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o	ABB58380	22	307	ω.	14
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Drosophila melanog	ABB67300	22	299	79.9	24
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polypeptide	14	22	323	89.2	1385.5
Human adenine nucl	AAU10380	23	298	9	٠.

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Scoring table: Sequence: Perfect score: Title

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Database

ALIGNMENTS

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(first entry)

Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. 03-NOV-1998; 08-SEP-1999; (MITO-) MITOKOR. 03-NOV-1999; 11-MAY-2000 WO200026370-A2 Human adenine nucleotide translocator ANT1 sapiens. 98US-0185904. 99US-0393441. 99WO-US25883

Result No.

Score 1553

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructs. ANT is a nuclear encoded protein and a major component of CC inner mitochondrial membrane. It mediates transport of adenosine CC di/tri:phosphates across the mitochondrial inner membrane and also serves CC as an important molecular component of the mitochondrial permeability CC transition pore, a modulator of apoptosis. ANT is used to identify agents CC or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for CC regulating mitochondrial pore activity, for treating diseases associated CC with altered mitochondrial function, including Alzheimer's, Parkinson's CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial cencephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic CC epilepsy red ragged fibre syndrome. The present sequence is an CCC adenine nucleotide translocator ANTI from human brain.
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Matches
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             Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial core component; mitochondrial related disorder; canc Alzheimer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                            Human adenine nucleotide translocator-1 (ANT-1)
                                                                                                                                  07-SEP-2001
                                                                                                                                                                 AAU01198;
                                                                                                                                                                                                AAU01198 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent discloses a
                                                                                                                                                                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
                                                                                                                                                                                                                                                                                                                                                                            QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ 240
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)B; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atent discloses a method to produce adenine nucleotide transle
proteins or ANT fusion proteins using recombinant expression
ructs. ANT is a nuclear encoded protein and a major component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Page 172; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                transition (MTP) pore components responsible for mediating transport CC of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to component of the component interact component of the present invention relates to a novel nucletc acid component construct comprising a promoter operably linked to a cyclophroceptide encoding a mitochondrial pore component polypeptide component polypeptide component polypeptide component protein (GFP) or a FLASH sequence). The novel capture construct can alter mitochondrial membrane permeability components. The methods are useful for screening for agents that alter components. The methods are useful for screening for agents that alter components. The methods are useful for screening for agents that alter components of diseases associated with altered mitochondrial function or constructional cell survival, such as Alzheimer's disease, diabetes components parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
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Velicelebi
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                              SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQ
                                                                                QGIIIYRAAYEGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ 240
                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV
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G, Davis RE;
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3.2e-173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
cc proteins mediate the exchange of ATP synthesised in the mitochondrial
cc matrix for ADP in the cytosol. (I) is useful for producing recombinant
cc ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
cc ulturing the host cell. (I) is also useful for targeting a polypeptide
cc of interest to a mitochondrial membrane, where ANT polypeptide is
cc expressed as a fusion protein with the polypeptide of interest.
cc expressed as a fusion protein with the polypeptide of interest.
cc expressed as a fusion protein that binds to an ANT polypeptide, is
cc useful for identifying an agent that binds to an ANT polypeptide. ANT
cc ligand is useful for determining the presence of an ANT polypeptide,
cc preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
cc valently bound to a solid phase. Detectably labeled ANT ligand is also
cc useful for identifying an agent that interacts with an ANT polypeptide.
cc the present sequence represents the amino acid sequence of human ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 44; Fig 2; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000; 2000US-0569327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10378;
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181 QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQ
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                                                                                          GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV
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Pei
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1553; DB 23; Pred. No. 3.2e-173;
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MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR

60

Matches Query Match Best Local

hes 279;

Similarity

93.9**%**; 93.6**%**;

Score 1457.5; DB Pred. No. 5e-162;

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RESULT 4
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                                         The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate. ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                            Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                            Disclosure; Page 39-40; 61pp; English
                                                                                                                                                                                                                                                                                                               gene
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N-PSDB; AAV36479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OxphOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
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                             independent
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                               of ANT1.
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(ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; A adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; c mitochondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                     against
                                                                                                                                                                                                                                                                                                                                                            Recombinant construct polypeptide, useful e.
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08-SEP-1999;
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                                                                                                                                                                                                                                 patent discloses a
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                                                                                                                                                                                                                                                                                                                                     nant construct encoding adenine tide, useful e.g. in screening f mitochondrial disease
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                                                                                                                                                                                                                                                                                Page 172-173; 175pp; English.
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Szabo
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                                                                                                                                                                                                                                                                                                                                                            agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dystonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
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New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.

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                                                                                                                                                                                                                                                    mitochondrial permeal mitochondrial core control allower's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders, mitochondrial diabetes and deafness (MIDD), and mepilepsy red ragged fibre syndrome. The present sequence is adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Huntington's diseases, cancer, psoriasis, usawere, grand Huntington's diseases, cancer, psoriasis, usawere, grand Leber's hereditary optic neuropathy, schizophrenia, mitochondrial Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative encephalopathy, lactic acidosis and deafness (MIDD), and myoclonic
                                                                                                                                                                                                                                                                                                                            07-SEP-2001
                                                              N-PSDB;
                                                                                           Murphy AN,
Velicelebi
                                                                                                                                               03-NOV-1999;
                                                                                                                                                                   03-NOV-2000;
                                                                                                                                                                                                            WO200132876-A2
                                                                                                                                                                                                                                                                                   Human; adenine
                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                 AAU01199;
                                                                                                                                                                                                                                                                                                                                                                    AAU01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with altered mitochondrial function, including Alzheimer's, Parkinson' and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
                                                                                                                          (MITO-)
                                                                                                                                                                                       10-MAY-2001.
                                                                                                                                                                                                                                  Homo
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                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-291054/30.
DB; AAS05902.
                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                       adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                          MITOKOR
                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                           G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AA;
                                                                                                    Clevenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                   2000WO-US30535
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                   core component;
isease; diabetes
                                                                                                                                                                                                                                                                         permeability transition
                                                                                                                                                                                                                                                                                                      nucleotide translocator-2 (ANT-2)
                                                                                           Davis
                                                                                                                                                                                                                                                                                   nucleotide
                                                                                                                                              99US-0434354
                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                                   translocator-2;
                                                                                                     Wiley
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                                                                                                                                                                                                                                                                                                                                                                     298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1391.5;
Pred. No. 2.7e
L7; Mismatches
                                                                                                                                                                                                                                                   ansition pore component; cell survival; mitochondrial related disorder; cancer; mellitus; hyperproliferative disorder.
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                                                                                                     Andreyev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 2:
                                                                                                                                                                                                                                                                                    ANT - 2;
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                                                                                                     ΑY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                   MTP;
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Disclosure;

Fig 2; 186pp; English

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzhered mitochondrial function or mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins intera with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid
                                                                                                                                                                                        mitochondrial
                                                                                                                                                                                                                                                                                                                                 AAU10379 standard; Protein;
   (MITO-) MITOKOR
                                11-MAY-2000; 2000US-0569327
                                                               11-MAY-2001; 2001WO-US15416.
                                                                                                                           WO200185944-A2
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                    Human adenine nucleotide translocator 2 (ANT2).
                                                                                                                                                                                                                                                                    14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression construct comprising a promoter operably linked to a polynuclectide encoding a mitochondrial pore component polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ANT-2) protein.
transition (MTP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human adenine nucleotide translocator-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. ANT) fused to an energy transfer molecule (ETM) protein
                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                            QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSD3IKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPKEQGELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEXQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263;
                                                                                                                                                                                                     adenine nucleotide translocator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                      matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANT proteins are mitochondrial permeability
                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.6%;
                                                                                                                                                                                                                                                                                                                                  298
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Pred. No. 2.7e-154;
7; Mismatches 16; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298;
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comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT cencoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ANT synthesised in the mitochondrial comprises the for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of culturing the host cell. (I) is also useful for targeting a polypeptide is compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion protein with the polypeptide of interest. Compressed as a fusion agent that binds to an ANT polypeptide. Compressed to suseful for determining the presence of an ANT polypeptide. Compressed as a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson (
Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant expression construct (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 44; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocator
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moos WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis
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Pei
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Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Szabo
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Matches
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                                                                                                                                                                            1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                     IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                         IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                          17;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                          1;
                    296
 297
                                                                                                                                                                                                          Gaps
                                          240
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Query Match Best Local

Similarity

89.6%;

Score 1391.5; DB 2 Pred. No. 2.7e-154;

23;

Length

298;

Sequence

298 AA;

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RESULT 8
AAY71033
ID AAY7
XX
AC AAY7
XX
DT 29-F
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DT UP-F
XX
DE Humm
XX
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                              Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; A adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; c mitochondrial permeability transition; neuroprotective; nootropic;
                                                                                                          Human adenine nucleotide translocator ANT3
                                                                                                                                                                                AAY71033;
                                                                                                                                                                                                                    AAY71033 standard; Protein;
                                                                                                                                              29-AUG-2000
                                                                                                                                          (first entry)
                                                                                                                                                                                                                    298
                  antidiabetic;
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neuroleptic

cancer;

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Matches
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Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, techev's hereditary out is neuroatthy schizophrania mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease - '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                           GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                      IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                               VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
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CK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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99US-0393441
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87.2%;
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Pred. No. 1.4e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is brain.
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04 DP OA

Query Match Best Local Matches 26

Similarity

89.2%; 87.2%;

Score 1385.5; Pred. No. 1.4e 21; Mismatches

1.4e-153;

DB

22;

Length

298;

Gaps

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RESULT 9
AAM39641
В
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                          system, such as peripheral nervous injuries, peripheral neuropathy; localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and the control of the activities such as: Immune system suppression, and the control of the activities such as: Immune system suppression, and the control of the activities such as: Immune system suppression, and the control of the activities such as: Immune system suppression, and the control of the activities such as: Immune system suppression, and the control of the activities such as:
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Wang
Zhao
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                                         C.N.S
                                                                    Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                           N-PSDB;
Sequence
                                                                                                                                                                                                                                                                      Example 4;
                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2000;
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19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-)
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DB; AAI58797.
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Wang 2
Zhou
                                        sequence
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298
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2000US-0598042.
2000US-0629312.
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2000US-0662191.
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2000US-0727344.
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The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MYTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU01200 standard;
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DB; AAS05903.
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G, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andreyev AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frigeri LG;
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RESULT 11
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Matches
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                                                                                                                         Anderson (Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alte MPT and/or cell survival. These agents are useful for the prevention treatment of diseases associated with altered mitochondrial function dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, mitochondrial encephalopathy, lactic acidosis, stroke,
                              Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                    WPI;
                                                                                     N-PSDB;
                                                                                                                                                               (MITO-) MITOKOR.
                                                                                                                                                                                        11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                11-MAY-2001;
                                                                                                                                                                                                                                           15-NOV-2001
                                                                                                                                                                                                                                                                   WO200185944-A2
                                                                                                                                                                                                                                                                                                                   mitochondrial matrix protein
                                                                                                                                                                                                                                                                                                                                Human; adenine nucleotide translocator;
                                                                                                                                                                                                                                                                                                                                                           Human adenine nucleotide translocator 3 (ANT3).
                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                            AAU10380;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10380 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                    2002-055598/07
)B; AAS16690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
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Moos
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                                                                                                                                     Davis
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                                                                                                                          , HW
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                          RE,
Pei
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                                                                                                                         Clevenger W, W
Y, Carroll AK;
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Pred. No. 1.4e
21; Mismatches
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                                                                                                                                     Wiley
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                                      for producing adenine nucleotide regulated promoter linked to
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                                                                                                                                        Miller
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Example 3; Fig

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English

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DT 22-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 260;
21-JAN-2000; 2000US-0488725
25-APR-2000; 2000US-0552317
09-JUL-2000; 2000US-0598042
                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; &By-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                  WO200153312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Pred. No. 1.4e-153;
1; Mismatches 16;
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RESULT 13 ABG15423

ABG15423

standard;

Protein;

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ABG15423;

Novel 18-FEB-2002

human

diagnostic protein

(first

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Matches 260
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                           localised neuropatries and central localised neuropatries and central sclerosis, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, Inhibin activity, chemotactic/Chemokinetic activity, haemostatic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the encoded polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                     Sequence
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ote: The sequence
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                                            GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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DB; AAI60583.
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                          IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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Wang Z
Zhou
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T, X
Goodrich R,
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87.2%;
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system injuries -
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Xu C,
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Pred. No. 1.6e-153;
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(u C, Xue
Drmanac R
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e AJ,
RT;
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2hang J;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, composition of the polymerase chain reaction (PCR) primers, oligomers, and for chromosome and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed content of the invention.
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food supplement;
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                     VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSV-TAVAGLLSYPFDT--VRRR 236
                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSD3LRGLYQGFNVS
IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFARNLASG
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upplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                     LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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Pred. No. 7.3e-143;
9; Mismatches 26; I
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                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL0187737-ABB72072).
                                                                                         Sequence
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                                                                                                                          The sequence data specification, but
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11-JUL-2000;
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                                           Similarity 79.7
32; Conservative
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2000US-0614150
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                                            79.9%; Score 1241; 1
79.7%; Pred. No. 1.20
tive 26; Mismatches
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                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form specification, but was obtained in electronic i
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11-JUL-2000;
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                            QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG 124
                                                                         AVGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE 66
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DB; ABL11403.
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Pred. No. 1.2e-136;
6; Mismatches 33;
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             GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 295
                                                                                                  IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
ATEVIYKNTLHCWATIAKQEGTGAFFKGAFSNILRGTGGAFVLVLYDEIKK 297
                                                  IYRAAYFGFYDTARGMLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRMMMQSGRK
                                                                                                                                                       QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG
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Search completed: November 12, 2002, 16:45:56 Job time: 30.9328 secs

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Minimum DB seg length: Maximum DB seg length:
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Listing first 45 summaries
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    No. is the number of results predicted by chance to have a
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is derived by analysis of the total score distribution.

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US-09-160-119-2
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US-09-501-558-2
US-08-933-750C-12
US-09-234-613-12
US-09-142-565-2
US-08-518-8788-56
US-08-518-8788-51
US-08-518-681-51
US-08-6470-868A-51
US-08-916-719A-51
US-08-975-009-32
US-08-977-09-32
US-09-172-528-2
US-09-318-199-2
US-09-318-199-2
US-09-318-199-2
US-09-318-75-64-4
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Sequence 10, Appl Sequence 4, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 56, Appli Sequence 56, Appli Sequence 51, Appli Sequence 32, Appli Sequence 32, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 56, Appli Sequence 56, Appli Sequence 56, Appli
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                                                                                                                                      ; MOLECULE TYPE: US-08-961-871-10
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                                                 Query Match
Best Local Sim
Matches 279;
                                                                                                                                                                                                TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Applicat Patent No. 6013858
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT IMFORMATION:
NAME: PETBET, DONNA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
APPLICANT: MacGregor Forant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder STATE: Colorado COUNTRY: US 2IP: 80303
                                                                                                                                                                                  TOPOLOGY:
    1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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US-08-946-719A-56
US-08-944-5228-36
US-08-518-878B-37
US-08-807-861A-37
US-08-946-719A-37
US-09-946-719A-37
PCT-US94-09799-1
US-08-933-750C-19
US-09-234-613-19
US-09-234-613-19
US-09-068-140A-15
US-09-318-199-6
US-09-318-199-6
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                                               Score 1457.5; DB 3;
Pred. No. 4.1e-161;
0; Mismatches 8;
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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

56, Appl 36, Appl 37, Appl 37, Appl 37, Appl 37, Appl 37, Appl 37, Appl 19,
Result

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Score

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Indels Length

Gaps

1:

298; <u>..</u>

Database

Sequence: Perfect score:

1553

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Scoring table:

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; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D.
                                                               454
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                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                               187 WRHL---VAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM-----CIVGGFTQM 233
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                                                                                                                                                                                                                                                                                                                                                                        234
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                                                                                                                                                                                                                                                                                                                                                                                         WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVV----RI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADP---GVFV-LLACGTISSTCGQLAS
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                                                                                                                                                                                                                                                   NVSVQGIIIYRAAYFGVYDTAKGM------LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227
                                                                                                                                                                                                                                                                                        LVAGSLAGATAQSSIYPMEVLKTRMAL----RKTGQYSGMLDCARRILAKEGVAAFYKGY 339
                                                                                                                                                                                                                                                                                                                            LASGGAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGF 176
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                                                                                                                                                                          YPFDTVRRRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFV- 286
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5. 6150502
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                                         ; TYPE: PRT
; ORGANISM: H
US-09-160-119-2
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                  SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application Patent No. 6316219
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Patent No. 6316219
                                                                                                                                                                    TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
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APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
                                                                                                                                                                                                                                                                                                                          APPLICANT: KRIEF, STEPHANE APPLICANT: SOUCHET, MICHEL APPLICANT: BRIL, ANTOINE
                                                                                                                                    NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
                                                                                                LENGTH: 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 RGNLANVIRYEPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCFV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGFLSFW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATYFPCYAHVKASFANEDGQVSPGSLLLAGATAGMPAASLVTPADVIKTR--LQVAARAG
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 18.7%;
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 291;
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Length 674;
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CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-501-558-2
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RESULT 6
US-08-933-750C-12
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US-09-501-558-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, C. Alexander Jr. APPLICANT: Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 YPLDFARTRL--AADV--GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                     233 VLRDGRCSGYTGTLDCLLQTWKNEGFFALYKGFWPNWLRLGPWNIIFFVTYEQLKK 288
                                                                                                       242 G-RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                     122 TIANPTDVLKIRMQA----QSNTIQGGMIGNFMNIYQQEGTRGLWKGVSLTAQRAAIVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555 QTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW 605
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                                                                                                                                                                              AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRMMQS 241
                                                                                                                                                                                                                                                       CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                                                                                                                                                                                                                                            ALYSGIAPAMLRQASYGTIKIGTYQSLKRLF...IERPED.-ETLPINVICGILSGVISS
                                                                                                                                                                                                                                                                                                                              SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                                                                                                                                                                                                                                                                   KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEIRYRGMLHALVRIGREEGLK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
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3; Mismatches 136;
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Pred. No. 1e-22;
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GENERAL INFORMATION:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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193
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CITY: Palo Alto
                                                                                                                                                                                                                                 72 RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCF 130
                                                                                                                                                                                                                                                                      20 VAGSVSGLVTRALISPEDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW
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                                                                                                                                                                                                 KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT
                                                                                        FGVYDTAKGMLPDPKNVHIFVSWMI-----
                                                                                                                          VHPVDVLRTRFAA----QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFPYAGLQ
                                                                                                                                                                                                                                                                                                                                                               Similarity
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Hillman, Jennifer L.
Bandman, Olga
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N: 536
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                                                                                                                                                                                                                                                                                                                                          15.3%; Score 238; DB 2; 23.5%; Pred. No. 2.8e-19; tive 67; Mismatches 124
                                                    HLY-KWAIPAEGKKNENLQNLLCGSGAGVISKTLTYPLDLFKK
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US-09-234-613-12
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Patent No.
                                                                                                                                                      Query Match 15.3%;
Best Local Similarity 23.5%;
                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN RI
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: September 2:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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         131 VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
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COMPUTER: IBM CON
OPERATING SYSTEM:
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CITY: Palo Alto
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CLONE: 207452
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                                  KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
                                                          RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCF 130
                                                                                      VAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW 79
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Bandman, Olga
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                                                                                                                                       67; Mismatches 124;
                                                                                                                                                      Score 238; DB 4;
Pred. No. 2.8e-19;
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                                                                                                                                                                 Length 320;
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        Sequence 56, Application US/08518878B Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
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US-09-142-565-2
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LENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 9705614.7 EARLIER FILING DATE: 1997-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
ORGANISM: HOMO SAPIEN
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                                                                                                                                                                                                                                            129 CFVYPLDFARTRLAADV----GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIII 185
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                                             SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                VNCAEVVTYDILKEKLLD
                                                                                                                                              YRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTA----VAGLLSYPFDTVRRRMMMQ 240
                                                                                                                                                                                            TCAQPTDVVKVRFQASIHLGPSRSDRKYSGTMDAYRTIAREEGVRGLWKGTLPNIMRNAI 191
                                                                                                                                                                                                                                                                                                                                          FWRGNLANVIRYFPTQALNFAFKDKYKQLFL-GGVDRHKQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                             FLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTARLVQYRGVLGTILTMVRTEGPCS
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---NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKR
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24.7%;
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US-08-470-868A-56
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                                                                                                                                                                                                                                                                                     Sequence 56, Application US/08470868A Patent No. 5861485
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Best Local Similarity
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                            TITLE OF INVENTION: Composition TITLE OF INVENTION: Treatment of the composition of the c
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 788
TELECOMMUNICATION INFORMATION:
                                                                                                                           NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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                                                            Pennie and Edmonds
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                                                                                                                                                      Compositions
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23.8%;
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2; Mismatches
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Pred. No. 4.8e-18;
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US-08-518-878B-51
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                                                                                                                                                                                                                                               Sequence 51, Applicat
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartag
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                       234 -NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                      ZIP:
                                                                                      STATE: New York COUNTRY: U.S.A.
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Local Similarity 23.8%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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PC-DOS/MS-DOS
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                                                                                                                                                                                                            COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS,
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Pred. No. 4.8e-18;
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US-08-807-861A-51
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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ACTERISTICS:

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TOPOLOGY:

100 ACTERISTICS:

100 ACTERISTICS
                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                   APPLICATION NUMBER: US/08/807,861A FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASK---QISAEKQYKGIIDCVVRIPKEQGFL 68
     APPLICATION NUMBER:
                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC 191
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                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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23.8%; Pred. No. 5e-18;
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US-08-470-868A-51
; Sequence 51, Application US/08470868A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5861485
GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
OUR APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
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STRANDEDNESS: sir
TOPOLOGY: unknown
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                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER:
                                                                                      FILING DATE:
                                                                                                             APPLICATION NUMBER: US/08/470,868A
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                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 131
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  Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                    New York
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23-AUG-1994
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06-JUN-1995
                                                                                   06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a, Louis C.
Compositions and Methods for the
Treatment of Body Weight Disorders,
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23.8%;
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Pred. No. 5e-18;
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Including Obesity

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09210681 atent No. 6057109
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 309 amino acid
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
08/807,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG
                                                                                                      APPLICATION NUMBER: US OF APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 -NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                 APPLICATION NUMBER: 08/6
FTILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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FILING DATE:
                           FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 FLGAGTAACIADLITEPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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1155 Avenue of the Amer
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(212) 869-8864
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                                                                                        US 08/470,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                      US 08/518,878
                                                                                                                                                                                                                                                                                                                                                         US/09/210,681
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Pred. No. 5e-18;
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SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:

Version #1.30

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

COMPUTER:

APPLICATION NUMBER: US/08/946,719A FILING DATE: 8-OCT-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/807,861 FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 0 FILING DATE: 23-AUG-1995

US 08/518,878 08/470,868

APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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RESULT 15
US-08-946-719A-51
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                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-97
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
              STREET: LLL STREET: New York
CITY: New York
""ATE: New York
" S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                        APPLICANT:
                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASK---QISAEKQYKGIIDCVVRIPKEQGFL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                    RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS----IGSRLLAGSTTGALAV
                                                                                                                                                                                                                                                                                                                 -NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 296
                                                                                                                                                                                                                                                                                                                                                                                   AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
                                                                                                                                                                                                                                                                                                                                                                                                                 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG
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RY: U.S.A.
10036-2711
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                                                                    1155 Avenue of the Americas
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                                                                                                                                                                        Tartaglia,
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                                                                                    Pennie & Edmonds LLP
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                                                                                                                          a, Louis A.

COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BODY WEIGHT DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 227; DB 3
23.8%; Pred. No. 5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148;
                                                                                                                                      DISORDERS,
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                                                                                                                                      INCLUDING OBESITY
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APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY_AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE_DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51
Search completed: November 12, 2002, 16:49:18 Job time: 12.9739 secs
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                                                                                                                                                                                                     192
                                                                                                                                                            189 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSG 242
                                                                                                                                                                                                                                                                                                                                           77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS----IGSRLLAGSTTGALAV 131
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                                                                                                                                    AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
                                                                                                                                                                                                                                                                                             SFWRGNLANVIRYEPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched
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                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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1553
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                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*

| (G9n2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| (G9n2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| (G9n2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| (C9n2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| (C9n2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| (C9n2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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                                                                                                                                                                                             /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
SUMMARIES
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677.670 Million cell updates/sec
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Result	Score	Query Match	Length	DB	ΙD	Description	
1	1553	100.0	297	10	US-09-811-094-31	Sequence 31, Appl	
2	1553	100.0	297	10		31,	
ω	1391.5	89.6	298	10	US-09-811-094-32	32,	
4	1391.5	89.6	298	10	US-09-810-644-32	32,	
ъ	1385.5	89.2	298	10	US-09-811-094-33	Sequence 33, Appl	
σ	1385.5	89.2	298	10	US-09-810-644-33	Sequence 33, Appl	
7	734	47.3	318	10	US-09-801-368-252	Sequence 252, App	
8	734	47.3	386	10	US-09-734-569-170	Sequence 170, App	
9	461	29.7	132	10	US-09-925-301-1459	Sequence 1459, Ap	
10	402.5	25.9	87	10	US-09-864-761-36440	Sequence 36440, A	
11	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appli	
12	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appli	
13	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appli	
14	304	19.6	469	9	US-09-992-598-289	289	
15	304	19.6	469	10	US-09-989-722-289	~	
16	304	19.6	469	10	US-09-989-723-289		
17	304	19.6	469	10	US-09-989-279-289	•	
18	304	19.6	469	10	US-09-989-727-289	Sequence 289, App	
19	304	19.6	469	10	US-09-989-731-289	Sequence 289, App	

5	44	43	42	41	40	39	38 8	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
212.5	214	220.5	227	231	233.5	233.5	233.5	234	238	240	244.5	246	251.5	258.5	266.5	275	288.5	304	304	304	304	304	304	304	304
13.7	13.8	14.2	14.6	14.9	15.0	15.0	15.0	15.1	15.3	15.5	15.7	15.8	16.2	16.6	17.2	17.7	18.6	19.6	19.6	19.6	19.6	19.6	19.6	19.6	19.6
272	275	379	309	309	312	312	312	309	320	323	131	436	410	433	310	289	342	469	469	469	469	469	469	469	469
10	10	10	10	10	10	10	10	10	10	12	10	10	10	10	9	10	10	12	10	10	10	10	10	10	10
US-09-796-766-14	US-09-808-457-4	US-09-810-673A-4	US-09-884-814-6	US-09-884-814-1	-457	US-09-826-507-2	US-09-734-134-2	US-09-884-814-8	US-09-840-787-12	US-10-006-867-126	US-09-925-300-1808	us-09-796-766-21	US-09-796-766-10	US-09-796-766-18	US-10-042-194-1	US-09-796-766-20	US-09-777-921A-6	US-10-006-867-58	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	US-09-989-732-289
Sequence 14, App	Sequence 4, Appl	Sequence 4, Appl	Sequence 6, Appl:	,1	Sequence 2, Appl:	Sequence 2, Appl:	Sequence 2, Appl:	Sequence 8, App	Sequence 12, Appl	Sequence 126, A	Sequence 1808, Ap	Sequence 21, Appl	Sequence 10, Appl	Sequence 18, App	Sequence 1, Appl.	Sequence 20, Appl	Sequence 6, App	Sequence 58, App	Sequence 289, A	Sequence 289, App	Sequence 289, A	Sequence 289, App	•	•	Sequence 289, App

ALIGNMENTS

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                                                                                                                                                                                                                                                                                    ; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31
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                                                                                                                                                                                                                                                                                             APPLICANT: MOOS, Walter H.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/09811094 Patent No. US20010044144A1
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 297; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, Chris
APPLICANT: Davis, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                    IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                      IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                            MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szabo, Tomas R. Ghosh, Soumitra Moos, Walter H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clevenger, William Wiley, Sandra Eileen Willer, Scott W.
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christen M.
                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                              Score 1553; DB 10;
Pred. No. 1.9e-154;
Mismatches 0;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                 Length 297;
                                                                                                                                                                                                              0;
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GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31
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                                                                                                               Sequence 32, Application US/09811094 Patent No. US20010044144A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Christen M APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 37 SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                             IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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Willer, Scott W.
Szabo, Tomas R.
Schosh, Soumitra S.
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US20020012992A1
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; LENGTH: 298
; TYPE: PRT
; ORGANISM: HOMO S
US-09-811-094-32
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                                                                  ; ORGANISM: Homo sapien 
US-09-810-644-32
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
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Matches
                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 32 LENGTH: 298
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SEQ ID NO 32
LENGTH: 298
Query Match
Best Local Similarity
Matches 263; Conserv
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Best Local Similarity
                                                                                                                                                                                                             TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (A TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
FILE REFERENCE: 660088.420D4
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                  LENGTH: 29
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                 89.6%;
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88.6%; Pred. No. 1.3e-137;
Live 17; Mismatches 16; I
 17;
Score 1391.5; DB 1
Pred. No. 1.3e-137;
7; Mismatches 16;
                                DB 10;
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
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5. US20010044144A1
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                                                                                                                                                                                                                                                                                            89.2%;
87.2%;
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                                                                                                                                                                                                                                                                                            Score 1385.5;
Pred. No. 5.5e
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US-09-801-368-252
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LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT:
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Best Local Similarity
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Patent No.
                                                                                                                                                                                                                                                         GENERAL
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APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/810,644
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Sounitra S.
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Pei, Yazhong
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No. US20020128250Alman, Thea
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Hecht, Peter
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Madden, Kevin
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; Pred. No. 5.56
21; Mismatches
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                                                                                              US-09-734-569-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 252
                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 170,
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Best Local Similarity
                                Matches
                                             Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                       PRIOR FILING DATE: 1999-1
NUMBER OF SEQ ID NOS: 181
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/171,101
                                                                                                                                                                                                                                                                TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lerchl, Jens
                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                           TYPE: PRT ORGANISM: Physcomitrella patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                           LENGTH: 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 LSLLFVYSLDYARTRLAADSKSSKKGGARQFNGLIDVYKKTLKSDGVAGLYRGFLPSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 TSLCFVYPLDFARTRLAAD----VGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKEEGYAKWFAGNLASGGAAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 GELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 NFLIDFLMGGVSAAVAKTAASPIERVKLLIQNQDEMLKQGTLDRKYAGILDCFKRTATQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ :|| || | | | ::::| ||:|| | :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156;
                                                                                                                                                                                                                                                                                                                              Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
                                                                                                                                                                                                                                                                                                               Reski, Ralf
                                                                                                                                                                                                                                                                                                                                                                             Frank, Markus
                                                                                                                                                                                                                                                                                                                                                                                        Bischoff, Friedrich
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52.9%;
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                             Score 734; DB 10;
Pred. No. 6.2e-69;
3; Mismatches 84;
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Pred. No. 4.9e-69;
5; Mismatches 82;
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                                                            Length 386;
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                              12;
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              RESULT 10
US-09-864-761-36440
; Sequence 36440, Application US/09864761
; Patent No. US20020048763A1
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GENERAL INFORMATION:
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; Sequence 1459, Application US//
Patent No. US20022052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Av.
; FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                       US-09-925-301-1459
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SEQ ID NO 1459
LENGTH: 132
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                 Best Local Similarity
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (126)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa
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LOCATION: (123)
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
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                                            61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRH 106
                                                                                                                       1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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IPKEQGVLSFWRGNLANVIRYFPTQALNFXFKDKYKQXFLXGVXKH
                                                                                            MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 85
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                                                                                                                                                                                                                 Score 461; DB 10;
Pred. No. 4.6e-41;
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the naturally occurring
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                                                                                                                                                                                                                                     Length 132;
                                                                                                                                                                                             Indels
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APPLICANT: Penn, Sharron G.

Hanzel, David I Chen, Wensheng

, David R. el, David K.

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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 36440
LENGTH: 87
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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FAGNLASGGAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRG 171
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                                                                                                                                                                                                                                                                                                                   D IN PLACENTA, SIGNAL = 1.9
D IN HEART, SIGNAL = 2.2
D IN HELA, SIGNAL = 7.3
D IN B7474, SIGNAL = 2.7
D IN ADULT LIVER, SIGNAL = 1.1
D IN BRAIN, SIGNAL = 2
THE TATE OF TAX BEAT OF TAX BE
                                                                                       Score 402.5; DB 10,
Pred. No. 3.4e-35;
Pred. Trohes 2;
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IN FETAL LIVER, SIGNAL = 2.3
IN BONE MARROW, SIGNAL = 1.5
                                                                                                                                                                                                                                                                  HIT: P05141, EVALUE 6.00e-38
HIT: AW935235.1, EVALUE 5.00e-37
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Query Match

22.3%;

Score

346.5;

DB 10;

Length 477;

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; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-2
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; LENGTH: 475
; ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4
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US-09-777-921A-2
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                                                                                            SEQ ID NO 2
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Patent No. US20020115136A1
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CURRENT APPLICATION NUMBER: US/09/777,921A

CURRENT FILING DATE: 2002-02-07
                                                                                                                                                        APPLICANT: MERKULOV et al.

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT PRILICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-07
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                                                                                                             NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 GAPQL -- NMVGLFRRIISKEGLPGLYRGITPNFMKVLPAVGISY -- VVYENMKQ 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 DLAVYELLKSHWLDNFAKDSVNPGVLVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 LWRGNGTNVIKIAPETAVKFWVYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLC 129
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95; Conservat
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Pred. No. 7.7e-29;
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US-09-992-598-289
Sequence 289, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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US-09-777-921A-5
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US-09-777-921A-5
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Best Local Similarity 34.6%;
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CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THERBOF
FILE REFERENCE: CL001103
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 410
TYPE: PRT
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                                                                                                                                                                                                      YFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPQL--NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY--VVYENMKQ
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                                                                                                                                                                                                                                         FIXPMEVMKTRLA--VGKTGQ--YSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI 353
                                                                                                                                                                                                                                                                                                           LWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT
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Pred. No. 6.6e-25;
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5; Mismatches 116;
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PRIOR APPLICATION NUMBER: 60/
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Stewart, Timothy A.
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PIR_73:*
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ts predicted by chance to have a	A; Status: preliminary A; Molecule type: DNA A; Residues: 1-298 < LIA>	
ne total score distribution.	R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-280, 1989 A;Title: DNA sequences of two expressed nuclear genes for A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03893	for human mitochondrial ADP/ATF
	A; Molecule type: DNA	
carrier nucleot		Wallace, D.C.
	Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987 A; Title: cDNA sequence of a human skeletal muscle AD	ADP/ATP translocator: lack of a lea
ADP, ATP carrier pr	A;Reterence number: A39891; MUID:88041149; PMID:2823 A;Accession: A39891	23266
ADP, ATP carrier	A:Status: preliminary A:Molecule type: mRNA	
ADP, ATP carrier	A; Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228	298 <nec></nec>
hypothetical	A; Experimental source: clone phMANT	
	R;Houldsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988	
ADP, ATP carri	A:Title: Two distinct genes for ADP/ATP translocase	se are expressed at the mRNA level incomes
hypothet	A; Accession: A28116	
	A: Molecule type: mRNA A: Residues: 1-37 <hou></hou>	
adp/atp	:J03593; NID:g339724; PIDN:A	AA36751.1; PID:g339725
ADP, ATP carrier	tal source: liver	
OB ADP, ATP carrier pr	A;Gene: GDB:ANT1; T1	
ADP, ATP carrier	A;Cross-references: GDB:119680; OMIM:103220	
hypothet	A; Map position: 4q35-4q35	
ADP,ATP carrier pr	C;Superiamity: ADP,ATP carrier procein; ADP,ATP carr C;Keywords: duplication; homodimer; mitochondrion; t	rrier protein repeat nomology
ADP, ATP carrier	F;2-298/Product: ADP, ATP carrier protein #status predicted <mat></mat>	
52 ADP,ATP carrier pr	F;110-202/Domain: ADP,ATP carrier protein repeat homero	homology <acp1></acp1>

298

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C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein C:Keywords: duplication; transmembrane protein F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>F:207-298/Domain: 
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A; Residues: 1-298 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I60173
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                                                                                                                                                                                                                                                                                                                                                                                                                              MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                     MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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                              QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                         VQGIIIYRAAYFGYYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                                                                           IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                            IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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  281;
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Pred. No. 1.6e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1466.5; DB 2
Pred. No. 4.3e-125;
9; Mismatches 7;
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                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change
C;Accession: A43646; A248422; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 198
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
                                                 A; Title: Bovine cardiac mitochondrial A; Reference number: A24822; MUID:86295 A; Accession: A24822
                                                                                                                            A;Cross-references: GB:M24102; NID:g529414; PIDN:/R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-298 < POW>
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A; Accession: S37210
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  A; Molecule type:
A; Residues: 208-2
                                                                                                                                                                                                                                                           A; Accession: A43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP,ATP.carrier protein T1 - bovine N;Alternate names: ADP/ATP translocase T1
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A; Residues: 1-298 <LAP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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208-298 <RAS>
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Pred. No. 8e-125;
Pred. No. 8e-125;
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                                                                             ADP/ATP-carrier: two 5775; PMID:3017341
                                                                                                                                                                                   PIDN: AAA30768.1;
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expressed

differently

22-Jun-1999

297

239

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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein C;Feywords: duplication; transmembrane protein C;Fey9/Domain: ADP,ATP carrier protein repeat homology <ACP1> E;I10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> E;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan11995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S37210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628
                                                                                                                                                                                                                                                                                           ;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Indels
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J. Biol. Chem. 262, 4355-4359, 1987
A; Title: Molecular cloning of a cDNA for a human ADP/ATP A; Reference number: A29132; MUID:87166056; PMID:3031073 A; Accession: A29132
                                         ADP,ATP carrier protein T2 - human

N;Alternate names: mitochondrial ADP,ATP translocase
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #t
C;Accession: A2913; C28116
R;Battini, R; Ferrari, S.; Kaczmarek, L.; Calabretta
J. Biol. Chem. 262, 4355-4359, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631 R; Aquilla, H.; Misra, D.; Eulitz, M.; Klingenberg, M. Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982 A;Title: Complete amino acid sequence of the ADP/ATP carrier from beef h A;Reference number: A03181; MUID:82188267; PMID:7076130
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A:Map position: Xq13-Xq26
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C:Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat homology C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein F:5-99/Domain: ADP.ATP carrier protein repeat homology <ACP1>F:110-202/Domain: ADP.ATP carrier protein repeat homology <ACP2>F:207-298/Domain: ADP.ATP carrier protein repeat homology <ACP3>
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A; Nolecule type: mRNA
A; Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A; Cross references: GB.J03591; NID:g339720; PIDN:AAA36749.
A; Cross references: Clone pHAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000
C;Accession: S03894; B28116
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A; Experimental source: C; Genetics:
                                             A; Molecule type: mRNA
A; Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A; Cross-references: GB:J03592; NID:g339722;
                                                                                                                                          R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
                                                                                                                                                                                                                                                                                                                             J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes f A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03894
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A; Residues: 1-298 <BA
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A; Residues: 1-298
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                                                                                                                          A; Accession: B28116
                                                                                                                                                                                                                                                                                                        A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Cozens, A.L.; Runswick, M.J.; Walker,
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Best Local :
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                                                                                                                                                                                                                                                        1-298 <COZ>
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Pred. No. 2.66
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                                                PIDN:AAA36750.1; PID:g339723
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A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat h C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: B43646
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43546
A;Status: preliminary
                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP,ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
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A; Residues: 1-298 < POW>
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F;207-298/Domain:
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                                                                                               IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                       MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
GAAGATSLCFVYPLDFARTRLAADVGKSGSEREFRGLGDCLVKITKSDGIRGLYQGFNVS
                                     GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                  Score 1380.5;
Pred. No. 2.6
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A;Cross-references: EMBL:x70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
C;Keywords: duplication; transmembrane protein
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%;Alternate names: adenine nucleotide translocase

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995

C;Accession: S31814
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F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                                                   MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLWQVQTNDRTITADKQYKGIIDCVVR
                                   QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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87.2%;
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Pred. No. 3.2e-116;
8; Mismatches 19;
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ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S31935; S31936 R;Beard, C.B.; Crews-Oyen, A.E.; Collins. F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 331777, CC;Ricession: 331777, Collins, K:HR;Beard, C.B.; Crews-Oyen, A.E.; Collins, K:HR;Beard, C.B.; Crews-Oyen, A.E.; Collins, K:HR;Beard, C.B.; Collins, K:HR;Beard, C.
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier C;Keywords: duplication; transmembrane protein F;7-101/Domain: ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S31935
A; Accession: S31935
                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-301 <BEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                        repeat homology
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S31935

mosquito)

#text_change 10-Sep-1999

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RESULT 10

RESULT 10

ry25850

hypothetical protein T01B11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T25850
R;Getsel, C: Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-313 <GEI>
A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Man-Cost-fice.4
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A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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                                                                                                                                         LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                     FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPEDTVRRRMMQSGRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSLCFVYPLDFARTRLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQVKGIIDCVVRIPKEQ
                                                                          AAYFGYYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                        LCFVYPLDFARTRLAADVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                                    LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                   FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVLVLVRVPKEQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRMMQSWPC
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DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                         AAYFGMFDTAKMVFTADGKKLNFFAAWAIAQVVTVGSGILSYPWDTVRRRMMMQSGRK--
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                                                                                                                                                                                                                                                                                                                             67.3%;
69.8%;
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                                                                                                                                                                                                                                                                                                              ; Score 1045.5; DB 2;
; Pred. No. 5.8e-87;
36; Mismatches 49;
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RESULT 12
T25371
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A; Residues: 1-300 <WIL>
A; Cross-references: EMB
                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z20024 A; Accession: T25371
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A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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A; Residues: 1-313 <WIL>
A; Cross-references: EMBL: Z68218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein K01H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
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T23207
                                                                    A; Map position: 3
A; Introns: 20/1; 4
C; Superfamily: ADF
                                                                                                                          C; Genetics:
A; Gene: CESP: T27E9.1
                                                                                                                                                                                                                                                                                                                                 C; Accession:
                                                                                                                                                                                                                                                                                                                                   hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T25371
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                                                                                                                                                                   A; Experimental source:
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               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPEDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCEVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
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                                                                       1; 41/3;
ADP,ATP
 Conservative
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                                                                                                                                                                     EMBL: Z82059; PIDN: CAB04874.1; ce: clone T27E9
                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BL:268218; PIDN:CAA92472.1; clone K01H12
                                                                       115/2
carrier protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carrier protein; ADP, ATP carrier protein repeat homology
               66.8%; Score 1037.5; 69.1%; Pred. No. 2.9
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                                                                       ADP, ATP
                 9e-86
                                                                       carrier
                                   DB 2;
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 49;
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Indels
                                 Length 300;
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RESULT 13
T15206
T15206
hypothetical protein W02D3.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_c
C; Accession: T15206
R; Le, T.; Weinstock, L.; Rifkin, L.
submitted to the EMBL Data Library, May 1997
A; Description: The sequence of C. elegans cosmid W02D3.
A; Reference number: Z18308
A; Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
 ADP, ATP carrier protein - Chl
C; Species: Chlorella kessleri
C; Date: 30-Jun-1992 #sequence
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A; Residues: 1-300 <LET>
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                                                                                                                                                                                                                                                                                                                         LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                     FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                               DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHLI
                                                                                                                                             DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                            AAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMMQSGRK---
                                                                                                                                                                                                                                                                      LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                       AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS 131
                                                                                                                                                                                                                                                                                                                                                                      FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                        LCEVYPLDEVRTRLGADVGKGVDREFQGLTDCFVKIVKSDGPIGLYRGFEVSVQGIIIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt AAYFGMFDTAKMVFASDGQKLNFFAAWGTAQVVTVGSGILSYPWDTVRRMMMQSGRK---}
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 #sequence_revision
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                                  Chlorella kessleri
                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Mismatches
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Pred. No. 2.3
 30-Jun-1992 #text_change
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F;209-301/Domain:
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QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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N;Alternate names: ADP/ATP transporter
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C;Accession: $68993; $51132
R;Hatin, I:; Jaureguiberry, G.
R;Hatin, I:; Jaureguiberry, G.
Fir. J. Biochem. 228, 86-91, 1995
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J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glycera A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Sratus. ....
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A:Molecule type: mRNA
A:Residues: 1-339 <HIL-7
A:Residues: 1-339 /Residues: 1-339 <HIL-7
A:Residues: 1-339 /Residues: 1-339 /Residues
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335 (;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; ADP,ATP carrier protein C;Reywords: duplication; transamebrane protein C;Reywords: duplication; transamebrane protein F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-301 <HAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Molecular characterisation of the A; Reference number: S68993; MUID: 95188918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP, ATP carrier protein - malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                      Local Similarity les 172; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
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                                        SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA--EKQYKGIIDCVVRIPKE
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NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE
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58.3%;
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                                                                                                                                                                  Score 904.5; DB 2;
Pred. No. 3.2e-74;
B; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                        protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                       Length 301;
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67
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Search completed: November 12, 2002, 16:48:36 Job time : 14.9686 secs

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"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
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ALIGNMENTS

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	(Rel. 12,
	<pre>01-NOV-1990 (Rel. 16, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)</pre>
	ier protein, heart/skeletal muscle isoform
	otide translocator 1) (ANT 1)
	ertebrata:
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	SEQUENCE FROM N.A.
	MEDLINE=89236396; PubMed=2541251;
	ਜਹ.E.;
	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
	J. Mol. Biol. 206:261-280(1989).
	SECTION OF PROM N. A.
	MEDLINE=89340499; PubMed=2547778;
	"A human muscle adenine nucleotide translocator gene has four exons,
	is located on chromosome 4, and is differentially expressed.";
	[3]
	SEQUENCE FROM N.A. MEDLINE=88041149; PubMed=2823266;
	ice D.C.;
	translocator:
	or a reader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";
	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
	SEQUENCE FROM N.A.
	TISSUE=Eye;
	R.;
	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. [5]
	SEQUENCE OF 1-37 FROM N.A.
	MEDLINE=88124845; PubMed=2829183;
	•
	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA
	roc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
	VARIANTS PEO PRO-114 AND MET-289.
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_	onen L., Suomalainen A.;
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DISEASE:
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ence 289:782-785(2000).
FUNCTION: CATALYZES THE EXCHANGE OF ADP MITOCHONDRIAL INURE MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
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sen the Swiss Institute of Bioinformatics
GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                         MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQI
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S; PR00926; MITOCARRIER.
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/FTId=VAR_012111.
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G -> A (IN REF. 3).
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                           TRANSMEM
REPEAT
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                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us entities requires a license agreement (See http
                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator."; Biochim. Biophys. Acta 1152:192-196(1993).
-1- FUNCTION: CATALYZES THE EXCHANGE OF ADD AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocase 1) (Adenine nucleotide SLC25A4 OR ANT1.
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Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                      EMBL;
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-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                  REPEAT
                                                                REPEAT
                                                                                                    TRANSMEM
                                                                                                                 TRANSMEM
                                                                                                                                                       TRANSMEM
                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                             InterPro; IPR002067; Mit_carrier
                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                        X61667; CAA43842.1;
D12770; BAA02237.1;
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                                                                                                                                                                                                        PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                             s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                          PS00215;
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                                                                                                                                                                                           MITOCH_CARRIER;
94.48;
                                                                                                                                                                               membrane;
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                                                                                                                                                                                                                                                                                                    is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
Score 1466.5; DB Pred. No. 7e-127;
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Sciurognathi; Muridae;
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                     between
the Euro
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Levy S.E., Chen Y.-S., Graham B.H., V

"Expression and sequence analysis of translocase 1 and 2 genes.";

Submitted (MAR-2000) to the EMBL/Geni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6; TISSUE-Brain, MEDLINE-97059403; PubMed-890: Ellison J.W., Li X., Francke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                     This
                                                                                                                                                               Strausberg R.;
Submitted (APR-2002) to
-!- FUNCTION: CATALYZES
MITOCHONDRIAL INNER
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Laplace C., Cos
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                                                                                                                                                                                                                               SEQUENCE FROM TISSUE=Eye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellison J.W., Li X., Francke U., Shapiro L.J.; "Rapid evolution of human pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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e European B
                                                                                 DOMAIN: COMPOSED OF SIMILARITY: BELONGS
                                                                                                                                  SUBCELLULAR LOCATION: Integral
                                                                                                                                                   SUBUNIT: HOMODIMER
                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation burdean Bioinformatics Institute. There are no restrictions on its
                                                                                                                   inner membrane.
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E MITOCHONDRIAL CARRIER FAMILY.
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Sciurognathi; Muridae;
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Query Match
Best Local 9
Matches 28
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EMBL; X74510; CAA52616.1; -.
EMBL; AF240002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC0026925; AAH26925.1; -.
MGD; MGI:1353495; S1C25a4.
InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR00193; Mitoch_carrier.
                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Ct
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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CONFLICT
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP
(Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                       ADT1_BOVIN
P02722;
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PRINTS; PR00926; MITOCARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
Mitochondrion; Inner membrane; Rep
Multigene family.
 SEQUENCE FROM N.A. MEDLINE=89229093; Powell S.J., Medd
                                                                                                                                            SLC25A4 OR ANT1.
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298
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PubMed=2540808;
S.M., Runswick
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EMBL; M24102; AAA30768.1;
PIR; A03181; XWBO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an unusually short 3'-noncoding sequence."; Biochem. Biophys. Res. Commun. 138:850-857(1986)-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two bovine differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry
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InterPro; IPR001993; Mitoch_carrier.
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"Bovine cardiac mitochondrial ADP/ATP-carrier: two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              норре-Seyler's Z. Physiol.
[3]
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hes 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A43646;
AGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQ
                                  DHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIP
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                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes for mitochondrial ADP/ATP translocase expressed
in various tissues.";
y 28:866-873(1989).
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                                                                                                                                                                                     Conservative
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MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
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f the ADP/ATP carrier
                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                  Mismatches
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les 8;
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P51881; O61311;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (/
EMBL; U27316;
EMBL; U10404;
EMBL; X70847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
Laplace C.
Submitted
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or send an
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the the EMBL outstation of the corporal Bioinformatics Institute. There are no restrictions on the corporal to the corporal t
                                                                                                                                                                                                                                                                                                                                                             Levy S.E., Chen Y.-S., Gr
"Expression and sequence
translocase 1 and 2 genes
Gene 254:57-66(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheldon J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=1
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MEDLINE=97059403; PubMed=8903724;
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                                                                           non-profit institutions as long
and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
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Eutheria;
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 AAC52838.1;
AAA19009.1;
CAA50196.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10974536;
                                                                                                                                                                                                                                                                                                                                                               yuence analysis of 2 genes.";
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Sciurognathi;
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                                                                                              (See http://www.isb-sib
                                                                                                                              There are no restrictions in as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocase
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RESULT 6
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ADT2 ADT3
AC 0090
DT 01-F
DT 01-F
DT 01-F
CC CC -!-
CCC -!-
CCC -!-
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                                                                                                                                                                                                                                                                                                                                                                              ADT2_RAT STANDARU;
019073;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, fibroblast isoform (## ADP_ATP carrier protein, f
                                                         SEQUENCE FROM N.A.

STRAIN-Sprague-Dawley: TISSUE-Liver;

MEDLINE-94002161: PubMed-8399300;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

Isolation and characterization of CDNA clones and a genomi encoding rat mitochondrial adenine nucleotide translocator.

Biochim. Biophys. Acta 1152:192-196(1993).

- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS MITOCHONDRIAL INNER MEMBRANE.

- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
TRANSMEM 12
TRANSMEM 73
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                          SLC25A5 OR ANT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF240003; AAF64471.1; ... MGD; MGI:1353496; Slc25a5.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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    SPECIFICITY:
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Rodentia;
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  PRESENT IN
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Pred. No. 1.4e
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                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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(POTENTIAL).
(POTENTIAL).
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KIDNEY,
                                        membrane
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  BRAIN,
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                                      protein. Mitochondrial
  HEART, LIVER AND
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RESULT
ADT2-HI
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ID 7-HI
DT 11:
DT 11:
DT 12:
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Best Local S
Matches 266
                                                                                                                                              T2_HUMAN STANDARD; PRT; 298 AA.

ADT2_HUMAN STANDARD; PRT; 298 AA.

P05141; 043350;
13-AUG-1987 (Rel. 05, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADI (Adenine nucleotide translocator 2) (ANT 2).

SLC25A5 OR ANT2.
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Mammalia; Eutheria;
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as 1
modified and this statement is not removed. Us
SEQUENCE FROM N.A. TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKELETAL MUSCLE.
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
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                                                             NCBI_TaxID=9606
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                                                                                                                            (Human)
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                                                                                      Primates;
                                                                                                        Chordata;
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16; Mismatches
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                                                                                 Craniata; Ve Catarrhini;
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                                                                                                          Vertebrata; Euteleostomi;
                                                                                   Hominidae;
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                                                                                                                                                                                         (ADP/ATP translocase
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EMBL; M57424; AAA51737.1; --
EMBL; J02683; AAA35579.1; --
EMBL; J02883; AAA35266.1; --
EMBL; AC004000; AAB96347.1; -
EMBL; J03591; AAA36749.1; -
PIR; A29132; A29132
PIR; C28116; C28116
 REPEAT
CONFLICT
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                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                         TRANSMEM TRANSMEM
                                                                                                                                            InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROCETTE: PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc.
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Becker M., Graves T.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90375457; PubMed=2168878; Ku D.-H., Kagan J., Chen S.-T., C The human fibroblast adenine nuc
                                        REPEAT
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: COMPOSED OF
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a R.A., Schlessinger D., Chen E.Y.;
(JUN-1996) to the EMBL/GenBank/DDBJ data)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibroblast adenine nucleotide translocator gene. Moleculid sequence.";
hem. 265:16060-16063(1990).
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                                                                                                                            Inner membrane;
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Best Local
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p1236; 096C49;

01-0CT-1989 (Rel. 12, Created)

01-NOV-1990 (Rel. 16, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

ADP, ATP carrier protein, liver isoform T2 (AD
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CONFLICT
SEQUENCE
                                                                                                                                                                                    Zhou J.,
Margolin
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=89236396; Cozens A.L., Runsw
                                     "Two distinct genes for ADP/ATP translocase level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(198-i-EUNCTION: CATALYZES THE EXCHANGE OF ADP
                                                                                                                             Strausberg
Submitted (
                                                                                                                                                                                                                           Cozens A.L., Runswick M.J., Walk
"DNA sequences of two expressed
ADP/ATP translocase.";
J. Mol. Biol. 206:261-280(1989).
                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   (Adenine nucleotide translocator SLC25A6 OR ANT3.
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                                                                                                                                                 TISSUE=Brain,
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                                                                                        MEDLINE=88124845; PubMed=2829183;
                                                                                                  ISSUE=Liver;
                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                             Submitted (JUL-2000)
                                                                                                                                                                                                          SEQUENCE
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         MITOCHONDRIAL INNER MI SUBUNIT: HOMODIMER. SUBCELLULAR LOCATION:
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298 AA;
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wick M.J., Walker J
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S THE EXCHANGE OF ADP AND
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                              MEMBRANE
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Pred. No. 1.26
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                                                                                                                                                                                                                                                                                                       Catarrhini;
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-> G (IN REF. 5).
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TRANSMEM 73
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TRANSMEM 117
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TRANSMEM 214
TRANSMEM 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
  01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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3L; BC008737; AAH088
3L; BC008935; AAH088
3L; BC014775; AAH148;
3C; S03894; S0389
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. J00592; AAA36750.1; -... J00592; AAG01998.1; -... BC007295; AAG07295.1; -... BC007850; AAH07850.1; -... BC008737; AAH08737.1; -... BC008935; AAH08935.1; -... BC014775; AAH14775.1; -...
                                                                                                                                                                                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300151;
                                                                                                                                                   VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSMMIAQSVTAVAGLLSYPFDTVRRRMM
||||||||||::|||||||||||
|VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSMMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                       IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260;
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IPR001993; Mitoch_carrier.
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                                             STANDARD;
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Pred. No. 1.8
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                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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-> F (IN REF. 3; AAH14775).
18534E9F0E49672F CRC64;
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1.8e-119;
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Matches 259
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MEDLINE-89229093; PubMed-2540808;

Powell S.J., Medd S.M., Runswick M.J., Wa
"Two bovine genes for mitochondrial ADP/I
differences in various tissues.";
Biochemistry 28:866-873(1989).
-!- FUNCTION: CATALYZES THE EXCHANGE OF I
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                      REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                      TRANSMEM
REPEAT
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TRANSMEM
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PTR; B43646; B43646.
InterPro; IPR001097; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP,ATP carrier protein, isoform T2 nucleotide translocator 3) (ANT 3). SLC25A6 OR ANT3.
                                                                                                                                                                                                                                                                                                                                                        Multigene
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                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00926; MITOCARRIER.
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181
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                                                                                                                                       DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane
                                            VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                 Similarity
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117
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214
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273
112
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32877
                                                                                                                                                                                                                                                                                                                                                                      membrane;
                                                                                                                                                                                      88.9%; Score 1380.5;
86.9%; Pred. No. 5.1
Live 21; Mismatches
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                    (POTENTIAL)
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ADP/ATP tr
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                                                                                                                                                                                       5.1e-119;
ches 17;
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RESULTANT AND STATE OF STATE O
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                REDLINE-2019(60)6; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Byans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Asbburner M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davanport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Cherry J.M., Cawley S., Dahlke C., Davanport L.B., Davies P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., McPherson D.,

RA Mount S.M., Mushon K., Mobarry C., Morris J., Moshrefi A.,

RA Notte B., Caller J.M., Murphy L., Muzny D.M., Nelson D.M.,

Rese M.G., Ra Palazzolo M., Barkon T., Shen H.,

Ra Chery J. M., Ra Ra Ra Ra Ra Ra Ra Ra Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y.Q.
Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT_DROME STANDARD; PRT; 297 AA Q26365; Q26254; P91614; Q9VZ70; Q259198 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular analysis of a candidate isolation between sibling species c experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster shows a high degree ADP/ATP translocases."; Mol. Evol. 35:44-50(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera,
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y
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MEDLINE=92389367; PubMed=1387687;
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EMBL; S71762; AAB31734.3; -
EMBL; Y10618; CAA71628.1; -
EMBL; AE003484; AAF47957.1;
FlyBase; FBgn0003360; sesB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenuation modified and this statement is not removed. Usage by
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-i- SUBCELLULAR LOCATION: Integral mem
inner membrane (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
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InterPro; IPR001993; Mitoch_carrier.
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GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                           ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                                                                                                                                QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
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                                        IYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRMMMQSGRK
                                                     IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK
                                                                                              ATSLCFYYPLDFARTRLAADTGKGGQREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGII
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79.4%;
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4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
1 -> Y (IN REF. 1)
R -> RG (IN REF. 2)
R -> TGA (IN REF. 2)
PC -> TGA (IN REF. 2)
PC -> S (IN REF. 2)
                                                                                                                                                                                                                                                              Score 1211; DB 1;
Pred. No. 1.6e-103;
5; Mismatches 33;
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C -> TGA (IN REF. 3 AND
-> S (IN REF. 1).
AA639439968F9750 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L11618; AAB04104.1; -.
EMBL; L11617; AAB04105.1; -.
InterPro; IPR001057; Mitcoh_carrier.
InterPro; IPR001993; Mitcoh_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94348635; PubMed-8069414; Beard C.B., Crews-Oyen A.E., Kumar V.K.,
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00926; MITOCARRIER. PROSITE; PS00215; MITOCH_CARRIER; 3.
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-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insect Mol. Biol. 3:35-40(1994).
-!- FUNCTION: CATALYZES THE EXCHANGE OF
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SUBUNIT: HOMODIMER (BY SIMILARITY).
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                                          TSLCFVYPLDFARTRLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
                                                                                    GIGAFWRGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLGSGGAAGA
                                                                                                  YGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCFVRIPKEQ
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Pred. No. 4.5e-99;
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the mosquito Anopheles
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Diptera; Nematocera;
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ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184

QGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLAG

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J. Biol. Chem. 266:24044-24047(1991).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Glucose increases the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00926; MITOCARRIER. 3. PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M76669; AAA33027.1; PIR; A41677; A41677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                    40
                                                                                              DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                    AFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00153; mito_carr;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001993; Mitoch_carrier.
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inner
                                                                                                                                                                                                                                                                           36686 MW;
                                                                                                                                                                                         62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                                                                       30;
                                                                                                                                                                                    Score 973.5; DB
                                                                                                                                                                                                                                                                                                                                               POTENTIAL).

(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Transmembrane; Transport.
(POTENTIAL).
                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
54779734A33B3942 CRC64;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP/ADP translocator
genes in Chlorella.";
                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP ACROSS THE
                                                                                                                                                                       Indels
                                                                                                                                                                                                                    Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                    99
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 밁
                                           Matches
                                                                 Query Match
                                                                                                                                                                                                 EMBL; X65194; .....
PIR; S30259; S30259.
InterPro; IPR002067; Mit_carrier.
ThterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADT_CHLRE
P27080;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLRE
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                                                                                                   TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure, evolution and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP, ATP carrier protein (ADP/ATP translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence up
01-OCT-1994 (Rel. 30, Last annotation
                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocator gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93204887; PubMed-8455552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-FUD44-R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                          SEQUENCE
                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                            PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3055;
                                                                                                                                                                        Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
                                                        Local
  7
                       7
                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Genet. 237:134-144(1993). FUNCTION: CATALYZES THE EXCHANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
          SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ
                                                                                                                                                                                                                                                                                                                                                                                     inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMMQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYRAAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGR
NEMVDFLAGGLSAAVSKTAAAPIERVKLLIQNQDEMIKQGRLASPYKGIGECEVRTVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI
                                                        Similarity
                                                                                                                                                                                PS00215; MITOCH_CARRIER; 2
                                                                                         308
                                                                                                     12
74
116
178
178
217
273
                                            Conservative
                                                                                         Ä
                                                                                                                                                                        Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Chlamydomonas
                                                                                                              29
92
133
197
234
                                                                                         33528
                                                       49.6%;
52.6%;
                                                                                                                                                                        membrane;
                                                                                          WW.
                                                                                                                                                                                                                                                                                                                                                                                                Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlorophyta;
                                            49;
                                                       Score 770.5;
Pred. No. 3.
                                                                                                 Repeat; Transmembrane; 1
(POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                         D477CF0E72B7A53F
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translocase)
                                                                                                                                                                                                                                                                                                                                                                                                membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                                                                                                                                                                       reinhardtii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the mitochondrial ADP/ATP
                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlorophyceae;
                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP
                                           1.4e-63;
nes 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP
                                                                                         CRC64;
                                                                 Length
                                            Indels
                                                                                                                                                                                                                                                                                              bу
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrial
                                                                                                                                                                      Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide
                                                                                                                                                                                                                                                                                               and
                                                                   308;
                                            17;
                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297
                                           Gaps
                                                                                                                                                                                                                                                                                               commercia.
                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
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RESULT
ADT1_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987
01-AUG-1992
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FNOT TIME TRANSPORTS AND THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MAIZE
ADT1_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leaver C.J., Bathgate B., Baker A.; "Two genes encode the adenine nucleotide translocator of mitochondria. Isolation, characterisation and expression
                                                                                                                                                                                                                                                          "Isolation and sequence analysis of a translocator of Zea mays L.";
Nucleic Acids Res. 13:5857-5867(1985)
-i- FUNCTION: CATALYZES THE EXCHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida;
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                    Baker A., Leaver C.J.;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85297781;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 70-387 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structural genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. B37N;
MEDLINE=89338399; PubMed=2547608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 59-387 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translocator from Zea mays L.";
Plant Mol. Biol. 17:305-307(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Panicoideae; Andropogoneae; NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translocase 1)
ANT1 OR ANT-G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP, ATP carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P04709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
                                                                                                                   SIMILARITY:
                                                                                                                                       DOMAIN:
                                                                                                                                                                                                                                  MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MAIZE
                                                                                                                                                               inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΚY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIVVYRGLYFGMYDSLKPVVLVGPLANNFLAAFLLGWGITIGAGLASYPIDTIRRRMMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIIIYRAAYFGYYDTAKG-MLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQ
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(Rel. 23, Last sequence update)
(Rel. 40, Last annotation update)
rier protein 1, mitochondrial precursor
1) (Adenine nucleotide translocator 1)
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EMBL; X15711; CAA33742.1; -.
EMBL; X02842; CAA26600.1; -.
PIR; A24072; A24072;
PIR; S05199; S05199.
PIR; S14876; S14876.
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                                               Schizosaccharomyces pombe (fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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InterPro; IPR001993; Mitoch_carrier.
                            Schizosaccharomycetales;
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Query Match
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EMBL; AL023634; CAA19176.1; -.
EMBL; AL023667; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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the European Bioinformatics Institute. There use by non-profit institutions as long a
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896,
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Gene 171:113-117(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER (BY SIMILARITY)
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93
131
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222
                                                 AA;
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                                                                                              per membrane;
48 1
111 2
151 3
151 3
217 4
242 5
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                                                 MW;
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Score 752.5;
                                                                                         Repeat; Transmembrane; Transport.
(POTENTIAL).
(POTENTIAL).
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13; Gaps
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Search completed: November 12, 2002, 16:46:26 Job time: 8.6495~secs

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Result
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Perfect score:
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                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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sp_bacteria:*
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sp_mhc:*
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sp_human:*
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1 062164
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046373 oryctolagus
062164 mus musculu
08sqh5 bos taurus
09yic4 rana rugosa
09prh1 rana rugosa
09prh2 rana rugosa
09im9 xenopus lae
095vx4 ethmostigmu
09nhw5 lucilia cup
091336 rana sylvat
041094 drosophila
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ALIGNMENTS

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Query Match 94.3%; Score 1464.5; DB 6; Length 298; Best Local Similarity 94.6%; Pred. No. 6.2e-126; Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60	Inner membrane; Mitochondrion; Transmembrane; Transport. SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;	Pfam; pF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER. PROCITE: DEGO075; MITOCARRIER. 3	<pre>InterPro; IPR001993; Mitoch_carrier. InterPro; IPR002067; Mit carrier.</pre>	-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. EMBL: AB009386: BAA23777.1; -	 -I - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY). 	J. Biochem. 335:541-547(1998).	regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle.":	"Identification of a 30kDa calsequestrin-binding protein, which	VAMBAQIICHI N. KARAIM M.	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9986;	Wammalia: Enthomia: Taxomorpha: Toporidae: Ormotolacus	Oryctolagus cuniculus (Rabbit).		(TrEMBLrel.	01-JUN-1998 (TremBirel 06, Created)		LT 1 73 046373 PRELIMINARY; PRT; 298 AA.

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RESULT 10.016 AC 20.016 AC 20.016 AC 20.016 AC 20.016 AC 20.017 D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Matches 280;
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Q62164;
                                                                                          InterPro: IPR00193; Mitcoh_carrier.
InterPro: IPR002067; Mit_carrier.
Pfam; PP00153; Mit_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE: PS00215; MITOCH_CARRIER; 3.
Hypothetical protein; Inner membrane;
Transport; Mitochondrion.
                                                                                                                                                                                                                        EMBL; X74510; CAA52616.1; --
EMBL; AF240002; AAF64470.1; --
EMBL; BC003791; AAH03791.1; --
EMBL; BC026925; AAH36925.1; --
MGD; MGI:1353495; Slc25a4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression and sequence analysis of the mouse translocase I and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).
SLC25A4 OR MANCI OR ANTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-MUSCLE; Laplace C., Costet P.; Submitted (SEP-1993) to the E
                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
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                                                                                                                                                                                                                                                                                                                    mitted (APR-2002) to the EMBL/GenBank/DDBJ databases SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITINUMER MEMBRANE (MY SIMILARITY).
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAN
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                     Pred.
                                      Score 1463.5;
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       Mismatches
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Best Local
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"Structural properties of mammalian mitochondrial ADP/ATP carrie identification of possible amino acids that determine functional differences in its isoforms.";
Mitochondrian 1:371-379(2002).
EMBL; AB065433; BAB84673.1; -.
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   Q9YIC4
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                                                                                                                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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267; Conserv
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   PRELIMINARY;
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Last annotation update)
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Best Local
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Mol. Biol. Evol. 15:1612-1619(1998).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHO INNER MEMBRANE (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY EMBL; AB008457; BAA36507.1;
InterPro: IPR001993; Mitoch_carrier.
                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
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InterPro; IPR002030; Mit_uncoupling
Pfam; PF00153; mito_carr; 3.
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Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99083429; PubMed-9866197;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic
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Ranidae; Rana
      n K.;
         chromosomes
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L Mol. Biol. Evol. 15:1612-1619(1998).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

INNER MEMBRANE (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER EMBL, AB008453: BAA36513.1;
-- REMBL; AB008453: BAA36513.1;
-- REMBL; AB008461; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008461; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008461; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008462; BAA36512.1;
-- REMBL; AB008461; BAA36512.1;
-- REMBL; AB0
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O9PRH2;
01-MAY-2000 (TIEMBLITEL 1:
01-MAY-2000 (TIEMBLITEL 1:
01-MAR-2002 (TIEMBLITEL 1:
                                                 INNER MEMBRANE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE MITOCHONDRIAL
EMBL; AB008460; BAA36510.1; -.
EMBL; AB008458; BAA36508.1; -.
EMBL; AB008459; BAA36509.1; -.
                                                                                                                                                                                                            MEDIINE-99083429; PubMed-9866197;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic s
Z, W, X, and Y in the frog Rana rugosa, inferred from
a sex-linked gene, ADP/ATP translocase.";
MOI. Biol. Evol. 15:1612-1619(198).

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                          InterPro;
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Pred. No. 5.7e-118;
Pred. No. 5.7e-118;
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                                                                                                                                                          A Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;

"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
Dynamic Patterns of Expression During Development.";

L Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
C INNER MEMBRANE (BY SIMILARITY).

-!- SUMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL, AF231347; AAF63471.1; --

R InterPro; IPR002097; Mit_carrier.

R FAINTS; PR00926; MITOCARRIER.

R PRINTS; PR00926; MITOCARRIER.

R PRINTS; PR00784; MTUNCOUPLING.

R PRINTS; PS00785; MITOCARRIER; 3.

PROSSITE; PS00785; MITOCARRIER; 3.
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O919M9;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
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Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea.
Xenopodinae; Xenopus.
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SEQUENCE 298 AA; 32940 MW; 91B740133751877F
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SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
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236; Conserv
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Last sequents that the contract of th
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Pred. No. 7e-1
25; Mismatches
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Q1-DEC-2001 (TrEMBLrel 19, C
Q1-DEC-2001 (TrEMBLrel 19, I
Q1-MAR-2002 (TrEMBLrel 20, I
GM12886p (LPO2776p).
SESB OR CG16944.
          SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Chawez C., Dorsett V., Farfan D., Frise E., George

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.

Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa

Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen 2., Fair J.A., Batterham P.;
"A cDNA clone encoding the AD/AFP translocase of Lucilia cuprina.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INDER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95S30
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EMBL; AF218587; AAF32322.1;
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-SS MAL SEEKING; Chen Z., Fair J.A., Ba
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
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     Submitted
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SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
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EMBL/GenBank/DDBJ databases
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Pred. No. 1.6e-105;
""Fmatches 36;
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Best Local Similarity
Matches 232; Conserv
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Q91336;
01-NOV-1996 (TrEMBLrel. C
01-MAY-1999 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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InterPro; IPR001993; Mitoch_carrier.

Pfam; PF00153; mito_carr; 3.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3.

SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP/ATP translocase.
Rana sylvatica (wood frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL; AY060978; AAL28526.1; EMBL; AY070894; AAL48516.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia; NCBI_TaxID=45438;
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Stapleton M., Brokstein
EMBL; U44832;
InterPro; IPR
                                                                                                                                Submitted
                                                                                                                                                                          TISSUE-LIVER;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial ADP/ATP
in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97398141; PubMed-9256066;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                            Q., Storey K.B.;
mitted (APR-1999) to the EMBL/GenBank/DDBJ
SUBCELL/LAR LOCATION: INTEGRAL MEMBRANE F
INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MITOCHONDRIAL
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                                                                                                   EMBL/GenBank/DDBJ databas
WTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n; Craniata; Vertebrata;
Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                    CARRIER FAMILY
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Ranidae; Rana
                                                                                                                                                                                                                                                                                                       translocase
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Park S.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER EMBL; AF025798; AAB87883.1; -. EMBL; AF025798; AAB87883.1; -. ENGLISH ENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TIEMBLIEL 06, 01-JUN-1998 (TIEMBLIEL 06, 01-MAR-2002 (TIEMBLIEL 20,
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PROSITE; pS00215; MITOCH_CARRIER: 3.
Inner membrane; Mitochondrion; Transs
SEQUENCE 317 AA; 35005 MW; 5F66B
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Inner membrane; Mitochondrion; NON_TER 288 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng L.-W., Comeron J.M., Genetica 0:0-0(1997).
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NCBI_TaxID=7237;
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QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                                          AIGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
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PF00153; mito_carr; 3.
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79.6%;
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Pred. No. 3.5e
25; Mismatches
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Pred. No. 7.66
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5F66B7ED8D5CEB72 CRC64;
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Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopteryyota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL EMBL; AF025799; AAB87884.1; -.
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                                                                                   ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
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a; Brachycera; Musc
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Cland R.A., Galle R.F., Roorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeitfer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Maril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C. Baldwin D., Botchan M.R., An H.-J., Andrews Pfannkoch C. Baldwin D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Ra Cherry J.M., Cawley S., Dahlke C., Ferriaz C., Ferriter S., Felschmann W., Ra Gebart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Classer K., Ra Harris M.L., Harvey D., Heinan T.J., Hernandez J.R., Feouck J., Ra Harris M.L., Harvey D., Heinan T.J., Hernandez J.R., Ketchum K.A., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.J., Ra Hostin D., Houston K.A., Li J., Li Z., Liang Y., Lin X., Lin X., Mattel B., McIntosh T.C., McIcod M.P., McBreson D.L., Ra Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Harris M.L., Harvey D., Heinan S., Pollard J., Puri V., Reese M.G., Ra McIntosh T.C., McIcod M.P., McBreson D.L., Weinsch D., Weinsch D.A., Weinstock G.M., Weissenbach J., Ra Sheng X.Y., McLodder R., Venter J., Wang X., H., Wang X., L., L., Lang G., Zhao Q., Zheng L., The State D., Pack
                   Query Match
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              062526 PRELIMINARY;
062526;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
ANT2 PROTEIN
ANT2 PROTEIN
                                                                                                                                                                                                   Zhang Y.Q., Davis A.W., Root
Submitted (MAY-1998) to the
EMBL; AE003484; AAF47956.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                             EMBL; Y10618; CAA71629.1;
FlyBase; FBgn002311; Ant2.
InterPro; IPR001993; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
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                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                     PF00153; mito_carr; 3.
S; PR00926; MITOCARRIER.
                                                                          PS00215; MITOCH_CARRIER; UNKNOWN_2
                                                          307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophilidae;
                                                        A
;
                                                        33744 MW;
                                                                                                                                                                                                                        W., Roote J., Ashburner M
to the EMBL/GenBank/DDBJ
73.9%;
73.8%;
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Last sequence update)
Last annotation updat
Score 1147;
Pred. No. 7
                                                        3D6B3DFD82061C0C CRC64;
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 7; DB 5;
7.5e-97;
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1D 1251299
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1D 2512
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Best Local
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                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Trans:
SEQUENCE 304 AA; 33307 MW; 51FD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Miya T., Makabe K., Satoh N.;
"Expression of a gene for major
translocase, during embryogenes!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q25129;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q25129
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D83069; BAA11765.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INNER MEMBRANE (BY SIMILARITY).

    ! - SUBCELLULAR

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roretzi."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7729;
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AGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQG
                                                                                                                                                                                WS---FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEQGFFSLWRGNLANVIRYFPTQALNFAFKDTYKKIFLAGVDKRKQFWRYFHGNLASGGA
                                                                                            KEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGA
                                                                                                                                                        WSAVDFAKDLAIGGTAAAISKTIVAPIERVKLLLQVQAVSTQMKAGTEYKGIIDAFVRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth Differ. 36:39-48(1994).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMVYKNTAHCWLVIAKQEGIGAFFKGALSNIIRGTGGALVLALYDEMKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAYFGFYDTCRDFLPNPKSTPFYVSWAIAQVVTTVAGIASYPFDTVRRRMMMQSGLKKS
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                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ne for major mitochondrial protein, ADP/ATP embryogenesis in the ascidian Halocynthia
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Pred. No. 3.66
8; Mismatches
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51FD0D7D6B654880
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annotation update)
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ches 54;
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30 CRC64;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                         score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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(first entry)

Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; notropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. 11-MAY-2000 (MITO-) MITOKOR 03-NOV-1998; 08-SEP-1999; 03-NOV-1999; WO200026370-A2 Homo sapiens. Human adenine nucleotide translocator ANT2. 98US-0185904 99US-0393441 99WO-US25883

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RESULT 2
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N-PSDB;
            mitochondrial permeal mitochondrial core co Alzheimer's disease;
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                                                          Human; adenine nucleotide translocator-2; ANT-2;
                                                                                          Human
                                                                                                                        07-SEP-2001
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DB; AAD00520.
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                                                                                        adenine nucleotide translocator-2 (ANT-2) protein.
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                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                        (first
                           e nucleotide translocator-2; ANT-2; MTP; cyclophilin;
permeability transition pore component; cell survival;
core component; mitochondrial related disorder; cancer;
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            mellitus; hyperproliferative
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                                                                                                                                                                                                                                                                                                                                                                                                    transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that al MPT and/or cell survival. These agents are useful for the preventit treatment of diseases associated with altered mitochondrial function dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polypucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                            Sequence
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sapiens.
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DB; AAS05902.
                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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3, Davis RE;
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Pred. No. 2.5e-154;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translocator polypeptides, nucleic acid encoding the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial matrix protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002
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                                                                                                                                                                                                                                                                                                     MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADK)YKGIIDCVVR
                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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DB; AAS16689.
VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                            IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                           MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                               IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Moos
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pei
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Y, Carroll AK;
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                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                1547; DB 23;
No. 2.5e-154;
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                           The patent discloses a method to produce adenine nucleotide translocator CC (ANT) proteins or ANT its an nuclear expression constructs. ANT is a nuclear encoded protein and a major component of constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine cd//ri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability cransition pore, a modulator of apoptosis. ANT is used to identify agents cor ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for cregulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, parkinson's cand Huntington's diseases, cancer, psoriasis, diabetes, dystonia, concephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative concephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative concephalopathy, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dyst diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeuti against mitochondrial disease \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; Adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; controchondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                        Claim 46; Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson CM,
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DB; AAD00521.
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                                               potential therapeutic agents
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Best Local
                                                                                                                            03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                               21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                Tang
Wang
 Example
                  Novel nucleic acids and such as central nervous
                                                        WPI;
                                                                                                                                                                                                                                               WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                     AAM39641;
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                                                                                                                                                                                                                               26-JUL-2001.
                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                           (HYSE-)
                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                   Leukaemia.
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                                                                       γT,
                                              2001-442253/47
DB; AAI58797.
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                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                                                polypeptide
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 4.
                                                                      Liu C
Wang Z
Zhou
                                                                                                           HYSEQ INC
 SEQ
                                                                                                                           2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
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I Z,
u P,
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 IJ
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Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                       Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.0%;
2786;
                 polypeptides, us
system injuries
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10078pp; English
                                                                                Chen R,
, Xu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1454; DB 21;
Pred. No. 1.5e-144;
3; Mismatches 9;
                                                                      len R, Ma
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Best Local S
Matches 274
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                                                                                                                                                                                                                                             Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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                                                                                                         03-NOV-2000;
                                                                                                                                                                              WO200132876-A2
                                                                                                                                                                                                                                                                                                                                     Human adenine nucleotide translocator-3 (ANT-3) protein.
                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU01200 standard; Protein;
                                    (MITO-) MITOKOR
                                                                      03-NOV-1999;
                                                                                                                                           10-MAY-2001
                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1PKEQGVLSFWRGNLANV1RYFPTQALNFAFKDKYKQ1FLGGVDKHTQFWRYFAGNLASG
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74; Conservative
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                                                                                                         2000WO-US30535
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92.6%;
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Pred. No. 1.5e-144;
3; Mismatches 9;
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Murphy AN,

Clevenger

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Wiley

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Frigeri

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability translation (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to creat the component of the protein cacid expression construct comprising a promoter operably linked to a code expression construct comprising a promoter operably linked to a component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein ce.g. ANT) fused to an energy transfer molecule (ETM) protein component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein compression construct can alter mitochondrial membrane permeability translition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter components. The methods are useful for screening for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for a that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 186pp; English.
 Homo sapiens
                                                   Human; adenine nucleotide translocator;
                                                                                                                    14-FEB-2002
                                                                                                                                                       AAU10380
                                                                                                                                                                                     AAU10380 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                  (first entry)
                                                                                    nucleotide translocator 3
                                 matrix protein
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nucleic acid ce encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide. CC isand is useful for determining the presence of an ANT polypeptide. CC ANT from a biological sample, where the ANT ligand is covalently or non-cc covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sin
Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide .
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Ghosh SS, M
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               QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                              MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
QSGRKGADIMYTGTVDCWRK1FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                               Similarity
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Pei
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Y, Carroll AK;
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Pred. No. 1.5e-144;
l3; Mismatches 9;
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypnucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, hemotactic/chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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CC and to produce other types of data and products dependent on DNA and consisted the product of the printed sequence data for this patent did not appear in the printed consistence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess
at ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti; Adenine nuclectide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
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N-PSDB; AAV36479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQEWRYFARNLASG
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                                                  Page
                                                                                                                                                                                                                                                                                         Macgregor
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                                               39-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerative muscle
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92.7%;
                                                                                                                                                                                                                                                                                         GR,
  the mouse Antl protein, the
                                               61pp; English
                                                                                                                                                                                                                                                                                              Wallace
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Pred. No. 1
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С.
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1.4e-140;
hes 15;
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Matches
                                             Query Match
                                                                                                                                            polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANTI
                                                                                        Sequence
                                                                                                                              independent of ANT1.
                        Local
    265;
                        Similarity
                                                                                        298
    Conservative
                                                                                        ΑĄ,
                        91.2%;
89.2%;
    15;
                                             Score 1411;
  Score 1411; DB 19;
Pred. No. 5.2e-140;
5; Mismatches 17;
  Indels
                                             Length
                                             298;
  0;
Gaps
  0
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241
                   241
                                          181
                                                                181
                                                                                      121
                                                                                                           121
                                                                                                                                 61
                                                                                                                                                       61
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                                                                                    QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                    VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                        MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                   297
                                          240
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                                                                                                                                                      120
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RESULT 11
AAY71031
AAY71031 standard; Protein;
 297
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Human adenine nucleotide translocator ANT1.

29-AUG-2000

(first

entry)

adenosine di phosphate; adenosine tri-phosphate; apoptosis; MPT; can mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neurolep antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystidiabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; Human; adenine nucleotide translocator; ANT1; ragged fibre syndrome mitochondria; ADP; ATP; neuroleptic; dystonia; cancer;

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myoclonic
Homo
sapiens.
                   epilepsy red
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WO200026370-A2

03-NOV-1998; 08-SEP-1999; 03-NOV-1999; 11-MAY-2000 98US-0185904 99US-0393441 99WO-US25883

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RESULT 12
AAU01198
ID AAU01
XX AU01
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XX O7-SE
XX U1000
XX U1000
XX Human
XX Human
XX Human
XX Hitco
KW Mitco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ANT) proteins or ANT fusion proteins using recombinant expression
constructs. ANT is a nuclear encoded protein and a major component of
constructs. ANT is a nuclear encoded protein and a major component of
constructs. ANT is a nuclear encoded protein and a major component of
constructs. ANT is a nuclear encoded protein and a major component of
constructs. ANT is mediates transport of adenosine
constructs are used to identify agents
constructed an important molecular component of the mitochondrial permeability
constructs. ANT is used to identify agents
constructed an important bind to, or interact with it. The ANT ligands are used to
detect or isolate ANT in a biological sample, and therapeutically for
construction interact with it. The ANT ligands are used to
construct or isolate ANT in a biological sample, and therapeutically for
construction interact with it. The ANT ligands are used to
construct or isolate ANT in a biological sample, and therapeutically for
construction interact with it. The ANT ligands are used to
construct or isolate ANT in a biological sample, and therapeutically for
construction interaction, including Alzheimer's, Parkinson's
and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
conserved the interaction interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interaction into the interact
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Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability translition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease
                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                                                                              AAU01198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATSLCFYYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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DB; AAD00519.
                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                           adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297
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                                                                                                           nucleotide translocator-1 (ANT-1) protein
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                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1391.5; DB 2
Pred. No. 5.9e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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> 241 180 181 121 121 61 61

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MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60

GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS

IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG MGDHAWSFLKDFLAGAVAAAVSKTAVAP IERVKLLLQVQHASKQISAEKQYKGIIDCVVR

120

60

VQGIIIYRAAYEGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPEDTVRRRMMM

240

QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY

```
The present sequence represents human adenine nucleotide translocator-1 (C (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to create MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a coplynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to an energy transfer molecule (ETM) protein (C (e.g. ANT) fused to a liter mitochondrial membrane permeability (e.g. ANT) fused to a second transition or the prevention or treatment of disease associated with altered mitochondrial function or dysfunctional cell survival. These agents are useful for the prevention or treatment of disease associated with altered mitochondrial function or dysfunctional cell survival. Such as Alzheimer's disease, disease, disease, disease, disease, disease, disease, disease, disease, disease as the content of the prevention of the prevention of the disease as the content of the disease as the content of the disease as the content of the disease as the content of the disease as the content of the disease as the content of the disease as the c
     Matches
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Velicelebi
                                                                                                                                               mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-2000;
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                            Similarity
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                                                                                                      297
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G, Davis F
  Conservative
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                          89.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
17;
                       Score 1391.5; DB 2
Pred. No. 5.9e-138;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SE,
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  16;
                                               22;
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                                               Length
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                                                                                                                                                                                                                                                 The invention relates to a recombinant expression construct (I) C comprising a regulated promoter operably linked to a nucleic acid CC comprising an adenine nucleotide translocator (ANT) polypeptide. ANT CC proteins mediate the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol: (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide. CC preferably ANTI, ANY2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-CC covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANTI.
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenine nucleotide translocator; ANT; mitochondrial matrix protein.
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS16688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITO-) MITOKOR
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              121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                Local
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                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                         IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                 297
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                89.9%;
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                                                                                                                                                                                Score 1391.5; DB 2
Pred. No. 5.9e-138;
7; Mismatches 16;
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                                                                                                                                                                                                                 297;
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RESULT 14
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                         polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating or disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disgnostics, forensics, gene mapping, identification or biological activity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human classification, but was obtained in electronic format directly from WIPO at fips, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 57415; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS91243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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263
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Query Match Best Local Similarity

87.0%; 99.2%;

Score 1346; DB 22; Pred. No. 3.1e-133;

Length

Sequence

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ARBSG0082
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                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABL18175) and the encoded proteins (ABBO1847-ABBJ2072).
                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct sequences
                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and interactions -
Sequence
                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
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pharmaceutical.
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                                      IIYRAAYFGFYDTARGMLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRMMMQSGR
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Search completed: November 12, 2002, 16:45:57 Job time: 31.0336 secs

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US-08-518-878B-37 US-08-807-861A-37 US-08-807-861A-37 US-08-910-681-37 US-08-910-681-37 US-08-910-681-37 US-09-068-140A-15 US-09-175-528-6 US-09-318-199-6 US-09-318-199-6 US-09-503-579-6 US-09-503-579-6 US-09-503-579-6 US-08-947-861A-56 US-08-947-861A-56 US-08-947-19A-56 US-08-945-719A-56 US-08-945-719A-56 US-08-945-719A-56 US-08-945-719A-56 US-08-945-719A-56 US-09-234-613-19 US-09-0861-140A-11	4	4	4	N	w	ω	N	υı	4	ω	N	N	4	w	ω	N	N	۳
	US-09-188-930-142	US-09-068-140A-10	US-09-234-613-19	US-08-933-750C-19	US-08-946-719A-56	US-09-210-681-56	US-08-807-861A-56	PCT-US94-09799-1	US-09-503-579-6	US-09-318-199-6	US-09-172-528-6	US-08-937-466-6	US-09-068-140A-15	US-08-946-719A-37	US-09-210-681-37	US-08-470-868A-37	US-08-807-861A-37	-08
	142, App		19, Appl	19, Appl	56, Appl	56, Appl		l, Appli			6, Appli	6, Appli	15, Appl	•	•	37, Appl	•	37, Appl

ALIGNMENTS

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-871-10
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US-08-961-871-10
Query Match
Best Local Similarity 89.2
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: FEIDER, Donna M.
                                                                                                                                                                                                                      TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBRAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                        NAME: Ferber, Donna M. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boulder
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Score 1411; DB 3; Pred. No. 2.8e-154; 5; Mismatches 17;

Length 298; Indels

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US-09-188-930-339
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Best Local S
Matches 86
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Munison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 1100.1011.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/188,930A
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                    VRRRWWWQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFV-LVLYD 292
                                                                                                                 PYAGIDLAVYETL-----KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASYPLAL
                                                                                                                                            IYRAAYFGIYDTAKGMLPDPKNTHI------VISWMIAQTVTAVAG-LTSYPFDT
                                                                                                                                                                                                                                                                                            RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM-----CIVGGFTQMIREG
                                                                                                                                                                                                                                                                                                                        KDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVV----RIPKEQ 65
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                                                                                                                                                                                                      TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII
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                                                        VRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYE
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461
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•RESULT 3

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SOFTWARE: FASTSEQ for Wi
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORCANISM: Homo sapiens
US-09-501-558-2
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; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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US-09-160-119-4
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                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09160119A Patent No. 6316219
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23 EARLIER APPLICATION NUMBER: EP 98401655.0
                                                                                                                                                                                                                                             APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
                                                                                                             EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4
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CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
                                                                                           SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                     APPLICANT: KRIEF, STEPHANE
                                 LENGTH: 447
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGILSGVISSTIANPTDVLKIRMQAQSNTIQG-----GMIGNFMNIYQQEGTRGLWKGVS
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
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APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: SOUCHET, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23 EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-160-119-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version
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                               245 KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGG-AFVLVLYDEIKKY 297
                                                                                                                                                           129 CFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 RAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 AIYFPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 IFTNPLEIVKIRLQV····-AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFS
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                                                                                                                                                                                                                                                                                 Local Similarity nes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 RGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKRTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                              FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMMQSGR
                                                                                                                               IFTNPLEIVKIRLQV-----AGEITTGPRVSALSVVRDLGFFGIYKGAXACFLRDIPFS
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RAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW
                                                               AIYFPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA 551
                                                                                              AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMQSGR
                                                                                                                                                                                               RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAGGCAGGSQV
                                                                                                                                                                                                                            RGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKRTQFWRYFAGNLASGGAAGATSL 128
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26.2%;
                                                                                                                                                                                                                                                                                                                                               16.9%; Score 261.5; DB 4; 26.2%; Pred. No. 3.2e-21;
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                                                                                                                                                                                                                                                                                                                                51; Mismatches 139;
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Pred. No. 1.7e-21;
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TYPE: PRT
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; ORGANISM: HOMO SAPIEN US-09-142-565-2
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FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER APPLICATION NUMBER: 970505.1
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
NUMBER: OF SEQ. ID NOS: 6
                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08775009 Patent No. 5935783
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                                                                                         APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: NO. 5935783el Genes Mapping in the
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal
NUMBER OF SEQUENCES: 45
                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 FDTVRRRMMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLV 289
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 TMVRTEGPCSPYNGLVAGLQRQMSFASIRIGLYDSVKQVYTPKGADNSSLTTRILA----
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l Similarity 24.8%;
76; Conservative 5
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; Pred. No. 4.5e-20;
56; Mismatches 149
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Region
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US-08-518-878B-51
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
ZIP: 1000 ... COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
TOWNTON IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/775,009 FILING DATE: 27-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                   APPLICANT: Tartaglia, TITLE OF INVENTION: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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TOPOLOGY: lir
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                                                            COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                STATE:
                                                                                                                 CITY:
                                                                                                                               STREET:
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REFERENCE/DOCKET NUMBER: CH
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                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDSR-----RGLLCGLGAGVAE
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1155 Avenue of the Americas
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28.1%;
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COMPOSITIONS AND METHODS

TREATMENT OF BODY WEIGHT
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Pred. No. 8.7e-20;
7; Mismatches 138;
                                                                                                                                                                                                   FOR THE DISORDERS,
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                                                                                                                                                                                                    INCLUDING OBESITY
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RESULT 9
US-08-807-861A-51
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08807861A Patent No. 5853975
                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Tartag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie &
                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 TYRRRMMMQS-GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PNVARNAIVNCAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VSVQGIIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212, TELEFAX: 66141 PENNIE
                                                                                                  COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                    STREET: 1155 A
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 LTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLL
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STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 23-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TDVPPTATVKFLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTI 66
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APPLICATION DATA:
                                                                                                                                    New York
                                                                                                                                                                    1155 Avenue of the Americas
                                                                                                                                                                                                                                                                         Tartaglia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : (212) 790-9090
(212) 869-9741/8864
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)N: 435
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In Release #1.0, Version #1.30
                                                                                                                                                                                                                        a, Louis A.

METHODS AND COMPOSITIONS FOR THE REGULATION OF BODY WEIGHT DISORDI

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                                                                                                                                                                                      Edmonds LLP
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                Version #1.30
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RESULT 10
US-08-470-868A-51
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                                                                                                                                                                                                                             Sequence 51, Application US/08470868A PATENT NO. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                 APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders,
NUMBER OF SEQUENCES: 56
                     COMPUTER READABLE FORM:
                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                291 YDEIKK 296
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STRANDEDNESS: sir
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   MEDIUM TYPE:
                                        COUNTRY: U
ZIP: 10036
                                                                             STATE:
                                                                                                              STREET:
                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VRIPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLA 118
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Local Similarity 23.5%;
les 72; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/470,868 FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/807,861A FILING DATE: 26-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVRRRMMMQS-GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVL 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGSTTGALAVAVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLL 121
                                                                                                                                                                                                                                                                                                                                                                           YEQLKR 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDVPPTATVKFLGAGTAACIADLITEPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTI 66
                                                                                             New York
                                                                           New York
                                                                                                              E: Pennie and Edmonds
1155 Avenue of the Americas
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Floppy disk
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Pred. No. 3.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/09210681 Patent No. 6057109
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                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Tartag
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                ADDRESSEE: Pennie a purion...
STREET: 1155 Avenue of the Americas
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nes 72; Conserv
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                                                                                                                                STATE:
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                                                                                                                              New York
                                                                                                                                                                                                                            Tartaglia, Louis A.
VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
Patentin Release #1.0,
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212) 869-8864
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23.5%;
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Pred. No. 3.2e-
8; Mismatches :
Version #1.30
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CURRENT APPLICATION DATA:

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Best Local Similarity
Vatches 72; Conserva
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: Sequence 51, Application US/08946719A
: Patent No. 6121017
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                                                                                                                 GENERAL INFORMATION:
APPLICANT: TATEAGIA, Louis A.,
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/470,868
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/294,522
APPLICATION NUMBER: US 08/294,522
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REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
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                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                   NUMBER OF SEQUENCES:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                ADDRESSEE:
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                                 New York
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New York
7: U.S.A.
                                               E: Pennie & Edmonds LLP
1155 Avenue of the Amer
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(212) 869-9741/8864
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                                                                                                                 COMPOSITIONS
DIAGNOSIS OF
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Pred. No. 3.2e-19;
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                                                                                                                 FOR THE TREATMENT AND BODY WEIGHT DISORDERS,
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Sequence 56, Application US/08518878B
Patent No. 5703902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 57
                                                                                                                               RESULT 13
US-08-518-878B-56
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-FEB-19
APPLICATION NUMBER: US
FILING DATE: 23-AUG-19
APPLICATION NUMBER: US
FILING DATE: 06-TUN-19
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APPLICATION NUMBER: U
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FILING DATE: 8-OCT-1997
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23.5%; Pred. No. 3.26
tive 58; Mismatches
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Pennie & Edmonds

of the

Americas

CITY: New York STREET:

New York 1155 Avenue

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US-08-470-868A-56
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 299 amino acids
                                                                                                                                                                                                              Sequence 56, Application US/08470868A Patent No. 5861485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/518,878B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Treatment of Body Weight Disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                             APPLICANT: Tartaglia, Louis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                  237 LGQ-----YSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 286
                                                                                                                                                                                                                                                                                                                                                                                                                       181 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVLVVKTRYMNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 CFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 FLAGGVAAAISKTAVAPIERVKLLLQVQHASK---QITADKQYKGIIDCVVRIPKEQEVL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 23-AUG-1995
                                                                                      STREET:
                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 66
                                                                                                                                                                                                                                                                                                                                                                                   -GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSL 128
USA
10036
                                                  New York
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COTUZZI, Laura A.
COTUZZI, Laura A.
70
                                                                                      1155 Avenue of the Americas
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                                                                                                        Pennie and Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
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US-08-775-009-32
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: COruzzi, Laura A.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          TITLE OF INVENTION: No. 5935783el Genes mapping in the TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal
                                                                                                                                                                                                                                                               APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 -GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 AAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMNQS 242
                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                            COUNTRY: U
ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                              32, Application US/08775009
o. 5935783
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                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 236.5; DB 2
23.6%; Pred. No. 6.8e-19;
                                                                                                                                                                                                                                                                                                    Beverly S.
                                                                                                                                                                                                             45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Critical Region
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SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-32
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Search completed: November 12, 2002, 16:49:19 Job time: 13.0131 secs
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FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3100
TELEPAX: (215) 568-3339
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.0%;
Best Local Similarity 27.8%;
Matches 84; Conservative 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            301 YK 302
                                                                                                                                                                                                                                                                                    182 -QGIIIYRAAYEGIYDTAKGMLPD-PKNTHIVISWMIAQTVTAVAGLTSY----PFDTVR 235
                                                                                                                            295 KK 296
                                                                                                                                                                                                                                                         194 NQAIRFF--VMTSLRNWYRGDNPNKPMNP-----LITGVFGAIAGAASVFGNTPLDVIK 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 FWRGNLANVIRYFPTQALNFA---FKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 KAILAGGLAGGIEICITFPTEYVKTQLQLDERSH----PPRYRGIGDCVRQTVRSHGVLG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 KDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEVLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDST-----RGLLCGLGAGVAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 232.5; DB 2; Length 311;
; Pred. No. 2.1e-18;
44; Mismatches 133; Indels 41; Gaps
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          111111111
987654
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1391.5
1391.5
752.5
741.5
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351
350
323.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/PCTUS.PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Compugen Ltd.
   Sequence 289, App
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                                                                                      Sequence 32, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 252, Appl
Sequence 252, App
Sequence 170, App
Sequence 1459, Ap
Sequence 36440, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
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US-09-810-673A-4	US-09-810-673A-6	US-10-006-867-126	US-09-796-766-21	US-09-808-457-4	US-09-796-766-18	US-09-840-787-12	US-09-796-766-10	US-09-884-814-6	US-09-884-814-1	US-09-884-814-8	US-09-808-457-2	US-09-826-507-2	US-09-734-134-2	US-09-925-300-1808	US-10-042-194-1	US-09-796-766-20	US-09-777-921A-6	US-10-006-867-58	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	05-09-989-/32-289
4,		•	Sequence 21, App.	4, 1	•	Sequence 12, Appl	10	Sequence 6, Appl:	Sequence 1, Appl:	Sequence 8, Appl:			Sequence 2, Appli	16	Sequence 1, Appli	Sequence 20, Appl		5	2	Sequence 289, App	•	Sequence 289, App	Sequence 289, App	-	sequence 289, App

ALIGNMENTS

RESULT 1 US-09-811-094-32

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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32
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Matches 298;
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 201-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anderson, APPLICANT: Davis, R
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APPLICANT:
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APPLICANT:
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                                                                                                                                             1 MTDAALSFAKDELAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQVKGIIDCVVR 60
                                                               IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
                                                                                                                              MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                           Similarity
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Wiley, Sandra Elleen
Willer, Scott W.
Szabo, Tomas R.
Scabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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Davis, Robert E.
                                                                                                                                                                                          Conservative
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US-09-810-644-32
; Sequence 32, Application U:
; Patent No. US20020012992A1
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                                         Sequence 33, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT:
APPLICANT:
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APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
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SOFTWARE: FastSEQ for Windows Version
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             Davis, Robert E.
Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
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Pred. No. 3.6e-154;
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                                                                   ; ORGANISM: Homo sapien US-09-810-644-33
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                                                                                                              CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
Query Match
Best Local Similarity
Matches 274; Conserv
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Best Local Similarity
Matches 274; Conserv
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
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                                                                                                                                                                                                           APPLICANT: MOOS, Walter H.
APPLICANT: Pe1, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Christen M. APPLICANT: Davis, Robert E. APPLICANT: Clevenger, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ghosh, Soumitra S.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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                                                                                                   LENGTH: 29
TYPE: PRT
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ORGANISM: Homo
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
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Ghosh, Soumitra S.
      Conservative
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Pred. No. 1.
                     Score 1454;
Pred. No. 1.
        Mismatches
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31
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RESULT
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Stabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
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                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                         GAAGATSLCEVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                              IPKEQEVLSFWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKRTQEWRYFAGNLASG 120
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Pei, Yazhong
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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                                                                                                                                                                                                                                                                 89.9%;
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                                                                                                                                                                                                                                                    Score 1391.5; DB 10
Pred. No. 6.4e-138;
Pred. No. 6.4e-138;
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; ORGANISM: Homo US-09-810-644-31
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US-09-801-368-252
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APPLICANT:
APPLICANT:
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Best Local :
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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                              APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                          APPLICANT: Busby,
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                                                                                                               Maxon, Mary
Milne, Todd
No. US20020128250Alman, T
Royer, John
Salama, Sofie
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Pei, Yazhong
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Ghosh, Soumitra S.
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Madden, Kevin
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Hecht, Peter
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SEQ ID NO 252
LENGTH: 318
                                                                                                                                                 SOFTWARE: Patentin
SEQ ID NO 170
LENGTH: 386
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PRIOR ETLING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR ETLING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                               TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US/60/171,101
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                                                                                                                                                                                                 PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
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ORGANISM: Saccharomyces
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SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQ-HASKQITADKQYKGIIDCVVRIPKEQ 65
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                                  al Similarity
157; Conserv
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Schmidt, Ralf-Michael
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Bischoff, Friedrich
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Ehrhardt, Thomas
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Pred. No. 4.4e-71
40; Mismatches 8
                               Score 741.5; DB Pred. No. 8e-70; 2; Mismatches
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Sequence 36440, Application US/09864761 Patent No. US20020048763A1
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SEQ ID NO 1459
LENGTH: 132
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (126)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (129)
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
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                                                                                                                       IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRT 107
                                                                                                                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 85
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                                                                                                         IPKEQGVLSFWRGNLANVIRYFPTQALNFXFKDKYKQXFLXGVXKHT
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Pred. No. 1.5e-43;
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GENERAL INFORMATION:

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                                                                      Matches
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OTHER INFORMATION: E
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKG 172
                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
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R INFORMATION:
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                                                                                                                                                                            INFORMATION:
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                                                                    ch 29.0%;
Similarity 100.0%;
87; Conservative
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N: EXPRESSED IN HBL100, SIGNAL = 1.0

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.9

N: EXPRESSED IN HEART, SIGNAL = 2.2

N: EXPRESSED IN HEART, SIGNAL = 2.7

N: EXPRESSED IN BTA14, SIGNAL = 1.1

N: EXPRESSED IN BTA14, SIGNAL = 1.1

N: EXPRESSED IN BRAIN, SIGNAL = 1.1
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                                                                 Score 448; DE Pred. No. 5.1 0; Mismatches
                                                                                                                                                                       P05141, EVALUE 6.00e-38
AW935235.1, EVALUE 5.00e-37
                                                                                                               DB 10;
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                                                                    Indels
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LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryctolagus
US-09-777-921A-4
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US-09-777-921A-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-2
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US-09-777-921A-2
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                                                                                                      GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
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                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09777921A
Patent No. US20020115136A1
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
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                       cuniculus
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                                                                                                                                                                                                                                             ENCODING HUMAN TRANSPORTER PROTEINS
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Query Match

22.6%;

Score 350;

DB 10;

Length 475;

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US-09-777-921A-5
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US-09-777-921A-5
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                                                                                                            RESULT 14
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Patent No. US20020115136A1

GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103

CURRENT APPLICATION NUMBER: US/09/777,921A

CURRENT FILING DATE: 2002-02-07
                                             Sequence 289, Application US/09992598 Patent No. US20020160384A1 GENERAL INFORMATION:
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Best Local Similarity
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              APPLICANT:
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SOFTWARE: FastSEQ
APPLICANT:
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                                                                                                                                                                                    AYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS
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                             Ashkenazi, Avi J.
              Baker, Kevin P
Botstein, David
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Pred. No. 4.3e-26;
""" matches 91;
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TITLE OF INVENTION: Secreted and Transmeml
TITLE OF INVENTION: Acids Encoding the S:
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087106
FILLING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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Stewart, Timothy A.
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DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/092182
DR FILING DATE: 1998-07-09
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R APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091544

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DR APPLICATION NUMBER: 60/091519

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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090472
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                                                                                                                        AYFGIYDTAKGM------LPDPKNTHIVISWMIAQTVTAVAG-LTSYPFDTVRRRMMM
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DR APPLICATION NUMBER: 60/089908
DR FILING DATE: 1998-06-18
DR APPLICATION NUMBER: 60/089947
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089948
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089952
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/090246
DR FILING DATE: 1998-06-22
DR FILING DATE: 1998-06-2

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DR APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

PR APPLICATION NUMBER: 60/089599

DR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089653

DR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089801

DR APPLICATION NUMBER: 60/089801

DR APPLICATION NUMBER: 60/089907

R FILING DATE: 1998-06-18

DR APPLICATION NUMBER: 60/089907

R FILING DATE: 1998-06-18

DR FILING DATE: 1998-06-18

DR FILING DATE: 1998-06-18

DR APPLICATION NUMBER: 60/089440

R FILLING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089512

DR FILLING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089514

DR FILLING DATE: 1998-06-16

DR FILLING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089532

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DR APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/08858
R FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-09 APPLICATION NUMBER: FILING DATE: 1998-0

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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-12

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OR APPLICATION NUMBER: 60/090252
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090254
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090349
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OR FILING DATE: 1998-06-23
OR APPLICATION NUMBER: 60/090429
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RESULT 15
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CÜRRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062186
PRIOR APPLICATION NUMBER: 60/065116
PRIOR APPLICATION NUMBER: 60/065111
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
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OR APPLICATION NUMBER: 60/06250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/08322
OR APPLICATION NUMBER: 60/08322
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087607
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OR APPLICATION NUMBER: 60/087607
OR APPLICATION NUMBER: 60/087607
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OR FILING DATE: 1998-06-02
DR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088025

PR FILING DATE: 1998-06-04

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Baker, Kevin P.
Botstein, David
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Godowski, Paul J.
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art, Timothy
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PRIOR OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088167
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DR FILING DATE: 1998-06-10
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              FVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRA 189
                                                     LWRGNGINVLKIAPESAIKFMAYEQIKR--LVGSDQET---LRIHERLVAGSLAGAIAQS 296
                                                                                                         RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASR----SNNMGTVGGFTQMTREGGARS
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                                                                     FWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLC 129
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ALIGNMENTS

A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3> RESULT 1
A29132
ADP,ATP carrier protein T2 - human
ADP,ATP carrier protein T2 - human
N;Alternate names: mitochondrial ADP,ATP translocase
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
ADP,ATP translocase 20 망 Вb Qγ В δÃ A;Cross-references: GDB:125190; OMIM:300150 A;Map position: Xq13-Xq26 A;Note: there may be some confusion in the A;Title: Two distinct genes for ADP/ATP translocase are expre A;Reference number: A94197; MUID:88124845; PMID:2829183 A;Accession: C28116 A;MoLecule type: mRNA A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247 R;Houldsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R. J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regular elements: A29132; MOID:87166056; PMID:3031073
A;Accession: A29132 C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C;Accession: A29132; C28116 A; Gene: GDB: ANT2; T3; C; Genetics: A; Experimental source: clone pHAT3 A; Molecule type: mRNA A; Residues: 1-298 <BAT> Query Match Best Local : Matches 181 121 Local Similarity es 298; Conserva Н 1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG Conservative 2F1 100.0%; Score 1547; DB 1; 100.0%; Pred. No. 3.8e-130; tive 0; Mismatches 0; Length 298; Indels expressed at the mRNA level PID: 9339721 0; Gaps 240 180 180 120 120 60 60 0, മ

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RESULT 3
B43646
ADP, ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
C;Accession: B43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:X70847
A; Cross-references: EMBL:X70847
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein o; Keywords: duplication; transmembrane protein
F; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP>F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
                                                                                                                           R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
B;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
A;Status: preliminary
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ADP,ATP carrier protein T2 - mouse
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A; Residues: 1-298 < POW>
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A; Residues: 1-298 <COS>
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                                                     MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                   IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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A;Cross references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GIC;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; transmembrane protein C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP,ATP carrier protein T3 - human N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes f. A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03894
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 36-104,'R',106,'A',109-298 <HOU:
A; Cross-references: GB:J03592; NID:g339722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S03894; B28116
                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: ANT3; ANT3Y
                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-298 <COZ>
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                                                                                      :110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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275; Conserv
                    Similarity
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                    94.0%;
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Pred. No. 3.2e-122;
Pred. matches 8;
                    Score 1454;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                   <UOU>
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7.3e-122;
hes 9;
                                             DB 1;
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Mismatches

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Gaps 60

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R:Oettmeler, W.; Masson, K.; Kalinna, S.
Eur. J. Blochem. 227, 730-733, 1995
A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADF A; Reference number: S69369; MUID:95172058; PMID:7867632
A:Accession: S69369
A:Molecule type: protein
A; Residues: 49-63:154-168 <OET>
C; Comment: This protein is synthesized in the cytosol and transported into the mitochond C; Complex: homodimer
C; Complex: homodimer
C; Complex: homodimer
C; Function: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A; Note: located in the inner mitochondrial membrane
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein; ADP, ATP carrier protein; homodimer; methylated amino acid; mitochd
E; 5-9yDomain: ADP, ATP carrier protein repeat homology <ACP1>
F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
F; 2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F; 52/Modified site: N6-methyllysine (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 208-298 < RAS>
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID
R; Aqulla, H; Misra, D; Eulitz, M; Klingenberg, M.
R; Aqulla, H; Misra, D; Eulitz, M.; Klingenberg, M.
R; Aqulla, H; Misra, D; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A; Title: Complete amino acid sequence of the ADP,ATP carrier from A; Residues: 2-51, /x', 53-70, /x', 72-109, /x', 111-298 < AQU>
A; Molecule type: protein
A; Residues: 2-51, /x', 53-70, /x', 72-109, /x', 111-298 < AQU>
A; Note: residue 52 may be methyllysine
A; Note: residue 52 may be methyllysine
B; Babel, W; Wachter, E; Aquila, H; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
B; Title: Amino acid sequence determination of the ADP,ATP carrie
A; Reference number: A61343; MUID:82046808; PMID:6271240
A; Accession: A61343
A; Molecule type: protein
A; Residues: 205-298 < GABS
B; Oettmeier, W; Masson, K; Kalinna, S.
Eur: J. Blochem. 227, 730-733, 1995
A. Title: (74)117-zeido-4-isporrovulacridone labels Cysisq of the
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XWBO

ADP,ATP carrier protein T1 - bovine

N;Alternate names: ADP/ATP translocase T1

C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier:
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M2410
R;Rasmussen, U.B.; Wohlrab,
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A;Gene: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein :
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: adenine nucleotide carrier C;Species: Mus musculus (house mouse) C;Date: 06-Jan-195 #sequence_revision 06-Jan-C;Accession: S37210 R;Laplace, C.; Costet, P. submitted to the EMBL Data Library, September A;Reference number: S37210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-298 <LAP>
A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                      QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                          GAAGATSLCEVYPLDEARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGENVS
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QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
                                                                                                                                                                                                                                   IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                     IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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267; Conserv
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Pred. No. 9.5e
6; Mismatches
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A44778; S03893; A3981; A28116
R;Li, K; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.;
J. Biol. Chem. 264, 13998-14004, 1989
J. Biol. Chem. 264, 13998-14004, 1989
A;Title: A human muscle adenine nucleotide translocator gene has four exons,
A:Reference number: A44778; MUID:89340499; PMID:2547778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein rC;Superfamily: transmembrane protein
C;Superfamily: ADP,ATP carrier protein protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
A;Status: not compared with A;Molecule type: DNA *A;Residues: 1-298 <COZ>
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Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of
A;Reference number: I60173; MUID:94002161;
A;Accession: I60173
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160173
                                                                    A;Title: DNA sequences of two expressed nuclear genes for human A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03893
                                                                                                                                      A;Cross-references: GB:J04982; NID:g178658; R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-280, 1989
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C; Date: 02-Aug-1996 #sequence_revision
                                                                                                                                                                                                                  A; Residues: 1-298 <LIA>
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A; Molecule type: DNA
                                                                                                                                                                                                                                                                                    A; Reference number: A44778; A; Accession: A44778
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A; Residues: 1-298 <R
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Pred. No. 1.4e-118;
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PMID:8399300
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                                                                                                                   ADP/ATP
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                                                                                                                                                                                                        ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936
C;Accession: S31935; S31936
C;Bacce, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier from
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R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP t: A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
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A;Map position: 4q35-4q35
C;Superfamily: ADP,ATP carrier protein; ADP,ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 A; Title: Two distinct genes for ADP/ATP translocase are A; Reference number: A94197; MUID:88124845; PMID:2829183 A; Accession: A28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-15,'A','17-146,'RR',149,151-226,'L',228-298 <NEC>
A;Cross-references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920
A;Experimental source: clone pHMANT
R;Houldsworth, J.; Attardi, G. 277-201 1000
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      Db
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A; Residues: 1-37 <HOU>
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Best Local
      241
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VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLVSYPEDTVRRRWMM
                                                                                                                                                                                                                                                                                      IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
                                                                                                                                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                                                                                                                                                                                 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.3%;
89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nrier protein; ADP,ATP carrier protein repeat homology homodimer; mitochondrion; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1413; DB 1; Pred. No. 3.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298;
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A; Reference number: S319;
A; Accession: S31935
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-301 <BEA> A;Cross-references: EMBL:Z21814; EMBL:Z21815 C;Superfamily: ADP,ATP carrier protein; ADP,ATP C;Keywords: duplication; transmembrane protein F;7-101/Domain: ADP,ATP carrier protein repeat repeat ADP, ATP carrier protein homology <ACP1> repeat homology

S31935

#text_change 10-Sep-1999

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mosquito

Anopheles

gambiae

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A;Map position: 3
A;Introns: 20/1; 41/3; 115/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: clone T27E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T27E9.I - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T25371
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Matches 225
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Best Local Similarity
Matches 203; Conserv
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           TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
                                                                                                                                                                                                                FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV
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                                                           RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKG
                                                                                                                                                                                                    FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMEVLIRVPKEQGV
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                                                                                                  LCFVYPLDFARTRLAADIGKAN-DREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY
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 -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKF
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225; Conservative
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                                                                                                                                                                                                                                                                   66.7%;
69.8%;
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78.1%; Pred. No. 1.40
Cive 18; Mismatches
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                                                                                                                                                                                                                                                                   Score 1032; DB 2; Pred. No. 2.8e-84;
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A; Map position:
A; Introns: 4/1;
C; Superfamily: A
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                                                                     a;cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
                                                                                                                                                                                                                                                                     hypothetical protein T01B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #te: C;Accession: T25850
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-313 <WIL>
                                                                                                                        A;Status: preliminary; 1
A;Molecule type: DNA
A;Residues: 1-313 <GEI>
                                                                                                                                                                                                R;Geisel, C.; Stellyes, L. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid A;Reference number: Z20099
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                                                      A;Gene: CESP:T01B11.4
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06; Conservative
 ADP, ATP
                191/2
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 carrier protein;
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70.8%;
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Pred. No. 5.5e-84;
8; Mismatches 53
                                                                                                                                                                from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             December 1995
                                                                                                                                                                                                                                                                                          15-Oct-1999 #text_change 11-Jan-2000
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                                                                                                                                                                GB/EMBL/DDBJ
 ADP, ATP carrier
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 protein repeat homology
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Local Similarity

206;

Conservative

28;

Mismatches

Indels

4.

Gaps

ų.

66.5%; Score 1029; DB 2; 70.8%; Pred. No. 5.5e-84;

DB 2;

Length

313;

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RESULT 14
A41677
ADP,ATP carrier protein - C'C;Species: Chlorella kessler: 30-Jun-1992 #seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13

P13206

hypothetical protein W02D3.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: T15206
R; Le, T; Weinstock, L; Rifkin, L.
Submitted to the EMBL Data Library, May 1997
A; Description: The sequence of C. elegans cosmid W02D3.
A; Reference number: Z18308
A; Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1
C;Superfamily: ADP,ATP carrier protein;
F;9-103/Domain: ADP,ATP carrier protein
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                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDB.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          8 FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESP: W02D3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                            RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKG
                                                                                                                                                                                                                                                                                                                               LSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCFVYPLDFARTRLAADVGKAN-EREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV
                                                                                                                                                               TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK
                                                                                                                                                                                            RAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMMQSGRK-
                                                                                                                                                                                                                                                                         LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                         FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
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                                                                                                                                                                                                                                                      LCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKF 312
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                                                                                                                                 -DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQ
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                            #sequence_revision
                                           kessleri
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                                                         Chlorella kessleri
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Pred. No. 3.5e-80;
2; Mismatches 58;
                            30-Jun-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP, ATP carrier
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                          #text_change
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                          20-Aug-1999
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A; Residues: 1-339 <HIL>
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-301 <HAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вp
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Best Local :
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                                        RIPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLAS
                                                                                                                                               Similarity
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C;Accession: R;Hilgarth, J. Biol. Che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Date: 07-May-1995 #sequence_revision C;Accession: S60993; S51132 R;Hatin, I.; Jaureguiberry, G. Eur. J. Biochem. 228, 86-91, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat hd
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
                                                                                                                                                                                                  F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACPF;209-301/Domain: ADP,ATP carrier protein repeat homology <ACPF
                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Molecular characterisation of the A; Reference number: S68993; MUID:95188918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP, ATP carrier protein - malaria parasite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG
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IIVYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLA
                                                                                                     Conservative
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65.8%;
                                                                                                                         60.6%;
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                                                                                        Pred. No. b.ue
3; Mismatches
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Pred. No. 1.6e-78;
9; Mismatches 64;
                                                                                                  Score 938; DB 2;
Pred. No. 6.6e-76;
3; Mismatches 67;
                                                                                                                                                                                                     protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-Sep-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP/ATP-transporter PMID:7883016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #text_change 09-Jun-2000
                                                                                                                                              Length 301;
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rch co time	241	239	181	180	122	120	63
Search completed: November 12, 2002, 16:48:37 Job time : 15.0157 secs	241 MMMSGRKGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQK 299	239 MWQSGRKG-TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296	181 SVTGIIVYRGSYFGLYDSAKALLETNDKNTNIVLKWAVAQSVTILAGLISYPEDTVRRRM 240	180 SVQGIIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRM 238	122 GATAGAISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGV 180	120 GGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNV 179	63 RYSKEQGYLSLWRGNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDESKFFCVNILS 121

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Q09073 rattus norv
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2 rattus norv
2 bos taurus
5 homo sapien
5 drosophila
8 anopheles 9
2 chlorella k
2 gossypium h
8 schizosacch
0 chlamydomon
0 saccharomyc
9 zea mays (m
3 neurospora
1 arabidopsis
7 zea mays (m
9 saccharomyc
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3 solanum tub
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7 arabidopsis
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bos taurus
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							095258 homo sapien				

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to CUITOG INDOM ON the to converte to the produced through a co	!- SIMILARITY: BELONGS TO THE MITOCHOND!	inner membrane. !- DOMAIN: COMPOSED OF	SUBCELLU	!- SUBUNIT: HOMODIMER.	MITOCHONDRIAL INNER MEMBRANE.	C. Natl. Acad. Sci. U.S.A. 85:377-381(1988).	ult human liver.";	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA	Houldsworth J., Attardi G.;	MEDLINE=88124845; PubMed=2829183;	iver;	SEQUENCE OF 47-298 FROM N.A.		Graves T., Ozersky P.;	ROM N.A.	Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.	Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R., Mazzarolla B.A. Schlessinger D. Chen F.V.:). BIOI. CHem. 262:4353-4356(1967).	л Л	"Molecular cloning of a cDNA for a human ADP/ATP carrier which is	Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,	SEQUENCE FROM N.A.	[2]	J. Biol. Chem. 265:16060-16063(1990).	ing and sequence.";	"The himan fibroblast adenine nucleotide translocator gene. Molecular	0375457; PubMed=2168878;	SPOTIPNON PROV N.A	NCBI_TaxID=9606;	ia; Primates; Catarrhini; Hominidae;	ryota; Metazoa; Chordata;	SLC25A5 OR ANT2.	(ANT 2).	ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)	UI-OCT-1994 (Rel. 30, Last appotation update)	13-AUG-1987 (Rel. 05, Created)	ADTZ_HUMAN STANDARD; PRT; 298 AA.	IAN	

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        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (...
(Adenine nucleotide translocator 2) (ANT 2).
                                                                                          RAT
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prints; pr00926; mitocarrier.
prosite; ps00215; mitoch_carrier; 3.
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                                                                                                                                               QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                                                         VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLISYPFDTVRRRMMM
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                                                                                                                                     QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
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                                                                                                                                                                                                                                                                      IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
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IPR001993; Mitoch_carrier.
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Pred. No. 9.4e
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                      (ADP/ATP translocase
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-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                         Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00926;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley;
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[1]
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                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                      IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                  IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
{\tt QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT}
                      QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                                              VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGLTSYPFDTVRRRMMM
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98.3%;
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2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
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There are no rest
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les 2;
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RESULT 3E
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                                                               EMBL; U27316; AAC52838.1; -.
EMBL; U10404; AAA19009.1; -.
EMBL; X70847; CAA50196.1; -.
EMBL; AF240003; AAF64471.1; -.
MGD; MGI:1353496; S1c25a5;
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_Carrier.
PRONSTE; PR00926; MITOCH_CARRIER; 3.
PRINTS; PR009215; MITOCH_CARRIER; 3.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase (Adenine nucleotide translocator 2) (ANT 2).
SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS.
Laplace C.
Submitted
                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restitute buropean Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20432087; PubMed=10974536;
Levy S.E., Chen Y.-S., Graham B.H., Wallace
"Expression and sequence analysis of the mou
translocase 1 and 2 genes.";
Gene 254:57-66(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U., Shapiro L.J.;
"Rapid evolution of human pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Skeletal muscle; Sheldon J.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-129/Sv;
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                                              Mitochondrion; Inner membrane; Repeat;
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81; Q61311;
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Eukaryota; Metazoa; C
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P32007;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, isoform T2 (ADP/ATP translocase nucleotide translocator 3) (ANT 3).
              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     Powell S.J., Medd S.M., Runswick M.J.
"Two bovine genes for mitochondrial a
differences in various tissues.";
Biochemistry 28:866-873(1989)
- PUNCTION: CATALYZES THE EXCHANGE
MITOCHONDRIAL INNER MEMBRANE.
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                                                                                                                                        Cozens A.L., Runswick "DNA sequences of two ADP/ATP translocase.";
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P12236; Q96C49;
O1-OCT-1989 (Rel. 12, Created)
O1-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP_ATP carrier protein, liver isoform T2 (ADP/ATP translocase
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SEQUENCE FROM N.A.
MEDLINE=89236396; PubMed=2541251;
MEDLINE=89236396; PubMed=2541251;
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PIR;
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                                                   YU W.,
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Biol. 206:261-280(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           level in adult human liver.";
proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: HOMODIMER.
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01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANC1).
SLC25A4 OR ANT1 OR ANC1.
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MGD; |
                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
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Submitted (APR-2002) to
-1- FUNCTION: CATALYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U., Shapiro I
"Rapid evolution of human pseudoautosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADT1
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SEQUENCE FROM N.A.
Chen Y.-S.,
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STRAIN-C57BL/6; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                  InterPro;
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                                                   L; U27315; AAC52837.1; ...
Li, X74510; CAA52616.1; ...
Li, AF240002; AAF64470.1; ...
Li, BC003791; AAH03791.1; ...
Li, BC026925; AAH26925.1; ...
Li, BC026925; AAH26925; AAH26925.1; ...
Li, BC026925; AAH26925; AAH2692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inner membrane
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   IPR002067;
IPR001993;
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Mitoch_carrier.
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THE EXCHANGE OF ADP AN
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                                                                             STRAIN-Sprague-Dawley, and Wistar; TISSUB-Heart MEDLINE-94002161; PubMed-8399300; Shinohara Y. Kamida M. Yamazaki N., Terada H. "Isolation and characterization of cDNA clones encoding rat mitochondrial adenine nucleotide to Biochim. Biophys. Acta 1152:192-196(193).
                                                                                                                                                                                                                   UD3902,
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
                             inner membrane.
-i- TISSUE SPECIFICITY: IN HEART,
                                                                                                                                                                      Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                               RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                 SLC25A4 OR ANT1.
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EXTENT, IN BRAIN AND KIDNEY DOMAIN: COMPOSED OF THREE HUSINILARITY: BELONGS TO THE J
                                                MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                       QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
||||| ||||||||||||||||
| QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
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                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                 Chordata;
Rodentia;
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89.6%;
 THREE HOMOLOGOUS DOMAINS.
TO THE MITOCHONDRIAL CARRIER
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                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                     ADT1_BOVIN STANDARD; PRT; 297 AA.

P02722;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
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EMBL; D12770; BAA02237.1; -.
InterPro; IPR001697; Mt_carrier.
InterPro; IPR001993; Mitoch_carrier.
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 MEDLINE=89229093; Powell S.J., Medd
                       SEQUENCE FROM N.A.
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PubMed=2540808;
S.M., Runswick
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PIR; A03181; XWBO.
PIR; A24822; A24822.
PIR; A43646; A43646.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153; mito_carr;
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Aquila H., Misra D., Eulitz M., Klingenberg N
"Complete amino acid sequence of the ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry
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InterPro; IPR001993; Mitoch_carrier.
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                      AAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSV
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Res. Commun. 138:850-857(1986)
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89.9%;
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363:345-349(1982)
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[2]
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MEDLINE-89236396; PubMed-2541251;
Cozens A.L., Runswick M.J., Walker J.E.;
"DNA sequences of two expressed nuclear
ADP/ATP translocase.":
                                                                                                                                                                                                                                                                               Strausberg R.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
                                                              Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Comi G.P., Keranen J., Peltonen L., Suomalainen A., "Role of adenine nucleotide translocator 1 in mtDNA Science 289:782-785(2000).
                                                                                                                    VARIANTS PEO PRO-114 AND MET-289.
MEDLINE=20385067; PubMed=10926541;
                                                                                                                                                                                     "Two distinct ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DLINE-89340499; PubMed=2547778; R., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., R., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., kuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.; human muscle adenine nucleotide translocator gene has four located on chromosome 4, and is differentially expressed."; Biol. Chem. 264:13998-14004(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol.
            MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral
                                                      FUNCTION: CATALYZES
                                                                                                                                                           distinct genes for ADP/ATP translocase are 1 in adult human liver.";
. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYFFDTVRRRMMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRMMMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
                                                                                                                                                                                                                                                                (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                      49; PubMed=2823266;
Li K., Wade R.P.,
                                                                                                                                                                                                Attardi
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                                                                                                                                                                                                              PubMed=2829183;
                                                      THE EXCHANGE OF
                                                                                                                                                        85:377-381(1988).
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             Mitochondrial
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
EMBL; BC008664; AAH08664.1; -.
PIR; A28116; A28116.
PIR; A38891; A39891.
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                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-i- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
-progressive external ophthalmoplegia with various mitochondrial
DNA deletions (PEO). Patients with PEO have mitochondrial
                                                                                                                                                                                                                                                                         VARIANT
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181
                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abnormalities associated with multiple different deletions mitochondrial DNA.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103220;
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                                                                                                                           GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                  A4477
         VQGIIIYRAAYEGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPEDTVRRRMMM
                                        GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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A44778; A44778.
VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
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/FTId=VAR_012111.

V -> M (IN PEO).

/FTId=VAR_012112.

G -> A (IN REF. 3)
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Pred. No. 1
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
ROSler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guban P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamm C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamm C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusxerin J., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wolf R., And H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,
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STRAIN=Oregon-R;
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
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Submitted (JAN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-92389367; PubMed=1387687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inner membrane (By similarity).
DOMAIN: COMPOSED OF THREE HOMOI
                                                                                                                                                                                               ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI
                                                                                                                                                                                                                                                                                    QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                         ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKE
  KATEVIYKNTLHCWATIAKQE
                                                                                                           IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGR
                                          KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                                                                                         ATSLCFVYPLDFARTRLAADTGK-GGQREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGI
                                                                                                                                                                                                                                                              QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                AVGFVKDFAAGQVSAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $43651; AAB23114.1; -. $71762; AAB31734.3; -. $710618; CAA71628.1; -. AE003484; AAF47957.1;
                                                                                    IIYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRMMMQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00153; mito_carr; 3.
S; PR00926; MITOCARRIER.
TE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
177
214
272
18
81
200
266
267
268
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75 93
119 136
77 196
2 290
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268
268
268
32880 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (IN REF. 1 I -> Y (IN REF. 1 I -> Y (IN REF. 1 I -> Y (IN REF. 2 G -> A (IN REF. 2 PC -> TGA (IN REF. 1 I -> Y GA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1218.5;
Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> A (IN REF. 2).

C -> TGA (IN REF. 3 AND.

-> S (IN REF. 1).

AA639439968F9750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein. Mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Ч , Wang
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י, Yao Q.A.,
י, Zheng י
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      124
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RESULT 11
ADT_ANOGA
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Best Local S
Matches 227
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gambiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrust;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT_ANOGA
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L11618; AABO4104.1; -. EMBL; L11617; AABO4105.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                  EMBL; L11617; AAB04105.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insect Mol. Biol. 3:35-40(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A cDNA encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94348635;
                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                    11 tochondrion;
                                                  128
 188
                                                                                                    83
                                                                                                                           10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                       inner membrane
                                      LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
RAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQSGRKGT
                                                                         GAFWRGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGHLGSGGAAGATS
                                                                                     LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS
                         LCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFNVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                       PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.B.,
                                                                                                                                                                                                                                                                                                                             PR00926; MITOCARRIER.; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                           14
75
119
178
216
275
301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crews-Oyen A.E.
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                             ; Inner membrane;
14 31 1
75 93 2
19 136 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8069414;
                                                                                                                                                                                                                                                    31
93
136
197
233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP/ATP carrier from
                                                                                                                                                                                                                              32863 MW;
                                                                                                                                                                                        76.9%;
78.8%;
                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Kumar V.K.,
                                                                                                                                                                                       Score 1190; DB Pred. No. 8e-99;
                                                                                                                                                                                                                                                                                        Repeat; Trans (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                           (POTENTIAL).
4CC9E17C9F8DA08B CRC64;
                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins F.H.;
the mosquito Anopheles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                            43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Adenine nucleotide
                                                                                                                                                                                                 Length 301;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrial
                                                                                                                                                                                                                                                                                                                 Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematocera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hexapoda;
                                                                                                                                                                           0
                                                                                                                                                                           Gaps
                                                187
247
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                                                                                                  127
                         189
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RESULT 12
ADT_CHLKE
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                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                     TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.",
J. Biol. Chem. 266:24044-24047(1991).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Glucose increases the expression of the ATP/ADP translocator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorella kessleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P31692;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADT_CHLKE
                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002067; Mit_carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A41677; A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M76669; AAA33027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
124
                                             99
                                                                                     64
                                                                                                                                     39
                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane
GATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLF-PKYSPKTDFWRFFVVNLASGGLA
                                                                                                                                                                                                                             194;
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                             45
108
151
209
248
304
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                        AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                     126
126
168
2528
265
322
36686
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65.8%;
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Pred. No. 5.6e
29; Mismatches
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(POTENTIAL).
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Shin H., Brown R.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U CUNA sequences for the adenine nucleotide translocator, T2, from cotton fibers (Gossypium hirsutum)."; ) Plant Gene Register PGR97-130.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochor membrane (B. Similarit.)
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                                                SFAIDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKSGRLSEPYKGIGDCFKRTIKDE
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                                                                                                                                    Score 771; DB
Pred. No. 2.4e
35; Mismatches
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Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Ra Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Ra Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Ra Holroyd S., Jones L., Jones M., Leather S., McDonald S., McLean J., Ra Mooney P., Moule S., Wungall K., Murphy L., Niblett D., Odell C., Ra Moliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Ra McLear S., Saunders D., Seeger K., Sharp S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Ra Sylaton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Ra Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Ra Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Garym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Giffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S., Ra Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J., Ra Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Sternows Section C. Schitzerches M., Narse P.; San The Recombs Section of Schitzerches M., Narse P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96257204; PubMed-8675018; Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.; Couzin N. Trezeguet V., Saux A.L., Lauguin G.J.M.; "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation saccharomyces cerevisiae.";
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
ANC1 OR SPBC530.10C.
        Cerrutti L., Lowe T., McCombie W.R., Paulsen
Shpakovski G.V., Ussery D., Barrell B.G., Nu
"The genome sequence of Schizosaccharomyces
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NCBI_TaxID=4896;
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Matches 158;
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Eukaryota; Viridiplar Chlamydomonadaceae; (NCBI_TaxID=3055; [1]
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                                                                             ADT_CHLRE STANDARD; PRT; 3
P27080;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence up
01-OCT-1994 (Rel. 30, Last annotation
ADP_ATP carrier protein (ADP/ATP trans
ADP_ATP carrier protein (ADP/ATP trans
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
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EMBL; AL023634; CAA19176.1; -
InterPro; IPR001267; Mt_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                    Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Pred. No. 2.3e-61;
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-i- FUNCTION: CATALYZES THE EXCHANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner membrane; Repea
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MEDLINE=93204887; PubMed=8455552;
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L Mol. Biol. Evol. 15:1612-1619(1998).

C -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDR INNER MEMBRANE (BY SIMILARITY).

C -: SINILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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R EMBL; AB008461; BAA35511.1; -.

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Best Local
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Mol. Biol. Evol. 15:1612-1619(1998).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROYONE INNER MEMBRANE (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CALEBEL; AB008450; BAA36510.1;

--- EMBL; AB008458; BAA36508.1;

--- EMBL; AB008458; BAA36509.1;

--- EMBL; AB008459; BAA36509.1;

--- InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.

pfam; PF00153; mito_carr; 3.

PRINTS; PR009256; MITOCARRIER.

PROSITE; PS00215; MITOCH_CARRIER: 3.

INDEX PROSITE; PS00215; MITOCH_CARRIER: 3.

INDEX PROSITE; PS00215; MITOCH_CARRIER: 3.

INDEX PROSITE: PS00215; MITOCH_CARRIER: 3.

INDEX PROSITE: PS00215; MITOCH_CARRIER: 3.
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Q9PRH2;
01-MAY-2000
01-MAY-2000
01-MAR-2002
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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MEDLINE-99083429; PubMed-9866197;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitof

"The origin and differentiation of the heteromorphic
Z, W, X, and Y in the frog Rana rugosa, inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Neobatrachia;
                                         Eukaryota; Metazoa;
Amphibia; Batrachia;
NCBI_TaxID=8410;
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  SEQUENCE
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Best Local S
Matches 271
                   Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage I
"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Spec:
Dynamic Patterns of Expression During Development.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCI
INUER MEMBRANE (BW SIMILARITY)
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMIL)
EMBL; AF231347; AAF63471.1; -.
InterPro; IPRO02067; Mit_Carrier.
InterPro; IPRO02067; Mit_Carrier.
InterPro; IPRO02067; Mit_Carrier.
InterPro; IPRO02030; Mit_Carrier.
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"The origin and differentiation of the heteromorphic sex chromosomes Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences c a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

-!- SUBCELLULAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL: AB008457; BA36507.1; -.

InterPro: IPR002067; Mit_carrier.

InterPro: IPR002030; Mit_carrier.

InterPro: IPR002030; Mit_uncoupling.

Pfam; PF00153; mito_carr; 3.

BETIMES: DED00256 mit_carrier.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
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PRINTS; PR00784; MTUNCOUDLING.
PROSTIE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Ti
SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
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NCBI_TaxID=8355;
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71; Conservative
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Pred. No. 2.6e
l6; Mismatches
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Matches 271
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Best Local
                                                                                                                                                   Matches
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INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CA
EMBL; AB009386; BAA33777.1; -
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mitoch_carrier.
PROSITE; PS00215; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER: 3.
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PRINTS; PR00784; MTUNCOUTLING.
PROSITE; PS00215; MITOCHOTION; Transmembrane; TI
Inner membrane; Mitochondrion; Transmembrane; TI
SEQUENCE 298 AA; 32940 MW; 91B740133751877F
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01-JUN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skeletal muscle.";
J. Biochem. 335:541-547(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
Yamaguchi N., Kasai M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                             Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                MSDQALSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                             membrane;
                                                                                                                                                                       Similarity
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. cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mitharia: Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                    Mitochondrion;
AA; 32901 MW;
                                                                                                                                                                     92.0%;
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91.6%;
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Last sequence Last anno
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Pred.
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Pred.
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                                                                                                                                                                                                                                      Transmembrane; Tr
CAEA32C88164AD78
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annotation
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No. 6
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No. 4.5e-118;
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                                                                                                                                                   .8e-118;
es 14;
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                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN. MITOCHONDRIAL
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7F CRC64;
                                                                                                                                                                                                                                        CRC64;
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                                                                                            Query
Best I
                                                                         Matches
                                                                                                                                                                                                                                -I- SIMILARITY: BELONGS TO THE MITOCHO EMBL; X74510; CAA52616.1; -. EMBL; R7240002; AAF64470.1; -. EMBL; BC003791; AAH03791.1; -. EMBL; BC003791; AAH03791.1; -. EMBL; BC026925; AAH26925.1; -. MGD; MGI:1353495; SIC2564.

InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002667; Mit_carrier.
Pf6m; PF00153; Mitoch_Carrier.
Pfam; PF00153; Mitoch_Carrier.
PROSTTE; PR00926; MITOCH_CARRIER; 3.
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Q62164;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy S.E., Chen Y.-S., Graham B.H., walle
"Expression and sequence analysis of the
translocase 1 and 2 genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
Chen Y.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=MUSCLE;
Laplace C. COstet P.;
Submitted (SEP-1993) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; (
                                                                                                                                                                     Transport;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-EYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                 Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
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                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE INNER MEMBRANE (BY SIMILARITY).
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                                                                         266;
                                                                                              Similarity
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                                                                                                                                                                Mitochondrion.
298 AA; 32904
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                                                                         Conservative
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Rodentia;
                                                                                              91.6%;
89.6%;
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                                                                                                                                                                   , WM
                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases.
NTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                    Score 1417; D
Pred. No. 2.3e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
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                                                                                                                                                                   3A849FEAB0981462
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                                                                                                                                                                                                              Repeat; Transmembrane;
                                                                                            .3e-117;
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                                                                                                                  Length
                                                                         Indels
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; Murinae; Mus
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                                                                      Gaps
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Best Local :
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                                                                                                                                                                                                                                                                                                                              MEDLINE=97398141; PubMed=9256066;
                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                               Amphibia; Batrachia; NCBI_TaxID=45438;
                                                                                                                                                                                                                                                                                                                                                                                                  ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                    091336;
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                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                   TISSUE-LIVER;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial
in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                         Rana sylvatica (wood
                                                                                                                                                       Inner membrane; Mitochondrion; SEQUENCE 317 AA; 35005 MW;
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181
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                 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
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VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                             Similarity
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                         frog).
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Last sequence update)
Last annotation updat
                                                                                                                      Pred. No. 1.60
4; Mismatches
                                                                                                                             Score 1295;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
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                                                                                                                                                      Transmembrane; Tr
5F66B7ED8D5CEB72
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.6e-106;
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372 CRC64;
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                                                                                                                      Indels
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Ranidae; Rana
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Best Local S
Matches 241
                                                                                                        Q95S30 PRELIMINARY;
Q95S30;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
GM12886p (LP02726p).
SESB OR CG16944.
                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inst
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Pleurostigmophora; SNCBI_TaxID=62613;
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burnell
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    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF401758; AAL02100.1; -.
Pro; IPR001993; Mitoch_carrier.
PF00153; Mito_carr; 3.
TE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
ENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E
                                                                                                                                                                                                                                                                                                               KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK
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Scolopendromorpha; Scolopendridae;
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                                              erygota; Diptera;
Drosophila.
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Last sequence up
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Ethmostigmus.
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Query Match
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Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AV060978; AAL28526.1; -.

EMBL; AV070894; AAL48516.1; -.

EIYBASE; FBG0003360; sesB.
SEQUENCE FROM N.A.
STRAIN-SS MAL SERKING;
Chen Z., Fair J.A., Batterham P.;
Chen Z., Fair J.A., Batterham P.;
"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AF218587; AAF33322.1; -.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                               Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco Oestroidea; Calliphoridae; Lucilia.
NCBI_TaxID=7375;
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InterPro; IPR001993; Mitoch_carrier.

Pfam; PF00153; Mito_carr; 3.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3.
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81.2%; Pred. No. 6.9e
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                   Eukaryota; Me
Pterygota; Ne
Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998
01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        044093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002067; Mit_carrier.

Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; MITOCARRIER.

PROSITE; PS00215; MITOCH_CARRIER; 3.

Inner membrane; Mitochondrion; Transmembrane; Transport.

SEQUENCE 300 AA; 33036 MW; 5459DF0EA0EZE742 CRC64;
                                                                                                                                                                                                                                                                Zeng L.-W., Comeron C
Genetica 0:0-0(1997).
                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                -i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL EMBL; AF025798; AAB87883.1; -. FlyBase; FBgn0023292; Dpse\sesB. InterPro; IPR001999; Mitoch_carrier. InterPro; IPR00267; Mit_carrier.
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                                                                                                                             Inner membrane; Mitochondrion;
                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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nes 237; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII
  QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
                         AIGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
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                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                             translocase
                                                                                                                                                                                                                                                                                      FROM N.A
                                                                                                                                                                                                                                                                                                                     pseudoobscura (Fruit fly).
Metazoa; Arthropoda; Tracheata; He
Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila.
                                                                                                                 288 AA;
                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence up
(TrEMBLrel. 20, Last annotation
                                                                                                                                                                                                                                                                         Comeron J.M.,
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
                                                                                                                  31725 MW;
                                                                               77.0%;
80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.7%; Score 1248.5; DB 5,
81.2%; Pred. No. 1.9e-102;
cive 20; Mismatches 34;
                                                                                                                                                                                                                                                                          Chen B.,
                                                                     20;
                                                                   Score 1190.5; DB
Pred. No. 2.5e-97;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                  052B0CC0050436B0 CRC64;
                                                                                                                                       Repeat; Transmembrane;
                                                                                                                                                   ω
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                                                                                                                                                                                                                                                    PROTEIN.
                                                                      33;
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                                                                                                                                                                                                                                                                                                                                Brachycera;
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Best Local
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                           INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CAI
EMBL; AF025799; AAB87884.1; -.
FlyBase; FB90023237; Dsub\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
PR0153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSTTE: PS00215; MITOCH_CARRIER: 3.
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Drosophila subobscura (Fruit fly).

Drosophila subobscura (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Francherygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng L.-W., Comeron J.M., Chen B., Kreitman Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              044094;
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                                                                                                                                                                                                                                                                                            Inner membrane; Mitochondrion; NON_TER 288 288 SEQUENCE 288 AA; 31775 MW;
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245
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KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
            KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLV
                                                                                                                                                            QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
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                                                                                                                                                                                             AMGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
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                                                                                                                                                                                                                                                         76.6%;
80.0%;
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Last annotation updat
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                                                                                                                                                                                                                                                        Score 1185.5; DB Pred. No. 6.9e-97;
                                                                                                                                                                                                                                                                                             06A1D1E477E81B26 CRC64;
                                                                                                                                                                                                                                                                                                                    Repeat;
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                                                                                                                                                                                                                                                                                                                  Transmembrane;
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Best Local S
Matches 221
                                                     062526 PRELIMINARY;
062526;
01-AUG-1998 (TrEMBLrel. (
01-AUG-1998 (TrEMBLrel. (
01-JUN-2001 (TrEMBLrel. 1
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Q25129;
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InterPro: IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Transpor
SEQUENCE 304 AA; 33307 MW; 51FD0D7D6B654880 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                  ANT2 protein.
ANT2 OR CG1683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stolidobranchia; Pyuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D83069; BAA11765
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL
                                                                                                                                                                                                                                       Growth Differ.
                                                                                                                                                       RNKEDRMYKGTVDCWGKIYKNEGGKAFFKGALSNVIRGTGGALVLVLYDELKK
                                                                                                                                                                RKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                                                                                                             IIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTYRRRMMMQSG
                                                                                                                                                                                                                                                                                                                              SAVDFAKDLAIGGTAAAISKTIVAPIERVKLLLQVQAVSTQMKAGTEYKGIIDAFVRIPK
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                 PRELIMINARY;
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ne for major mitochondrial
embryogenesis in the ascic
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                                                                                                                                                                                                                                                                                                                                                                                    74.0%;
75.4%;
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17, Last annotation
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Zhang Y.Q., Davis A.W., Nove.

Shamitted (MAY-1998) to the EMBL/GenBank/DDbu us

R EMBL; AE003484; AAF47956.1; .

R EMBL; Y10618; CAA711629.1; .

R FlyBase; FBgn0025111; Ant2.

JR FlyBase; FBgn0025111; Ant2.

InterPro; IPR01093; Mitoch_carrier.

DR InterPro; IPR002067; Mit_carrier.

DR PROSTE; PF00153; Mito_carr; 3.

DR PRINTS; PR00926; MITOCARRIER; UNKNOWN_2.

PROSTE; PS00215; MITOCH_CARRIER; UNKNOWN_2.

PROSTE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
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RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Hanck H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Horkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Gerphios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebabis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebabis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Harris N.I., Harvey D., Heiman T.J., Wei M.-H., Houck J.,
A Harris N.I., Harvey D., Heiman T.J., Wei M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Maron K., Nusskern D.R., Mesheri A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Trector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Spier E., Zhong F.N., Zhong W., Zhon W., Zhong L.,
RA Gibbs R.A., Wests E.M., Rubin G.M., Zhon W., Zhon S., Zho W., Smith H.O.,
RA Spier E., Shan M., Zhong G., Zhou X., Sm
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Matches 215
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NCBI_TaxID=7227;
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                                                                              VLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGAT
                                                                                                                                      SLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIII
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tive 27; Mismatches
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ALIGNMENTS

AAY71033 ID AAY7

AAY71033 standard; Protein; 298

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29-AUG-2000 AAY71033;

(first entry)

RESULT 1

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Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial dencephalopathy; lactic acidosis; stroke; MIDD; mitochondrial denbetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
(MITO-) MITOKOR
                                  03-NOV-1998;
08-SEP-1999;
                                                                                   03-NOV-1999;
                                                                                                                    11-MAY-2000
                                                                                                                                                     WO200026370-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Human adenine nucleotide translocator ANT3.
                                                                                                                                                                                    Homo sapiens.
                                  98US-0185904
99US-0393441
                                                                                   99WO-US25883
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dystonia;

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RESULT 2
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CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
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Ghosh SS;
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          Human: nootropic: immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                      Human
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DB; AAD00521.
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es 0;
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GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

180 180 IPKEQGVLSFWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG

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IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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N-PSDB; AAI58797.
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                                                                                         Sequence
                                                                                                              specification
                                                                                                                          Note: The
                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                   Zhao
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29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia
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                                                                                                                                                                                                                                                                       invention relates to human nucleic acids (AAI57798-AAI61369) encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                     S disorders.
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QΑ,
          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                            298;
                                                       Similarity
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                                                                                                                                                                                                                                                                                                                               central nervous
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Wang z
Zhou
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2000US-0553317.

2000US-0598042.

2000US-0598042.

2000US-0623312.

2000US-0663450.

2000US-0663191.

2000US-0693036.

2000US-0727344.
                                            Conservative
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Wehrman T,
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                                                                                                                                                                                                                                                                                                                              polypeptides, useful for system injuries -
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Xu C,
                                                      Score 1543; DB
Pred. No. 4.8e-1
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Yang Y,
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157;
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Matches 298
                                                                                                                                                                                                                     expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial porce component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or designated associated with altered mitochondrial function or the functional call survival such as altebrace of diseases.
                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MTP. The present invention relates to a novel nucleic acid
                                                                                                                               Sequence
                                                                                                                                                                         dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
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Velicelebi G,
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                                                                                                                                                             hyperproliferative
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2001-291054/30.
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               cc comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial cc matrix for ADP in the cytosol. (I) is useful for producing recombinant and cculturing the host cell. (I) is also useful for producing a polypeptide cculturing the host cell. (I) is also useful for targeting a polypeptide confinement of the form of the polypeptide is confinement. The polypeptide is confinement and polypeptide, or cells expressing the polypeptide. ANT cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion protein with the polypeptide of interest. Cc expressed as a fusion agent that binds to an ANT polypeptide. ANT cc useful for identifying an agent that interacts with an ANT polypeptide. Cc valently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
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Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
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Y, Carroll AK;
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RESULT 5
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                         Alzheimer's; Parkinson's disease; Huntington's disease; Huntington's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammatic-leukaemia.
                                                                                                                                                                                                                                                                                                                                                                      AAM41427 standard; Protein;
                                                                  Wang
                                                                                                                                                                                                                                                                                                                     Human polypeptide
      Novel nucleic acids and such as central nervous
                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                         WO200153312-A1
                                                                                                                                                                                                                                          Homo
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                                                                                           (HYSE-)
                                                                                                            29-NOV-2000;
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19-OCT-2000;
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                                                        J,
QA,
                                2001-442253/47
DB; AAI60583.
                                                                                                                                                                                                                                                                                                                                                                                                                QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                         Liu (
Wang 2
Zhou
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0652450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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u P,
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                                                                                           INC
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                                                        Asundi V,
Wehrman T,
Goodrich F
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6358
                                                                                                                                                                                                                                                                                                                                    entry)
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     polypeptides, useful
system injuries -
                                                               Chen R,
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lu C, Xue
Drmanac R
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e AJ,
RT;
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Yang Y,
               for treating disorders
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Zhang ,
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Qy

181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMTAQTVTAVAGVVSYPFDTVRRRMMM

240 205 180

VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

Qy В

В

266 241 206

QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298

Qy

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Вþ

146

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Db
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                                                                                                                                       Query Match
Best Local Sim
Matches 298;
                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activing inhibin activity, chemotactic/chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                              C.N.S disorders.
Note: The sequence specification.
                                                                                                                                                                                                               Sequence
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86
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                                                                                        1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                               323
                                                                                                                                         Conservative
                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                  data
                                                                                                                                                        100.0%; Score 1543; DB 22; 100.0%; Pred. No. 5.4e-157;
                                                                                                                                                                                                                                                                 for this
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145
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RESULT 6
AAY71032
ID AAY7
XX
AAC AAY7
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AC AAY7
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Huma
DE Huma
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; ine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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dystonia

cancer;

WO200026370-A2

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RESULT 7
AAU01199
ID AAU
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AC AAU
AC AAU
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DT 07-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine dlytri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDLAS), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson CM,
Ghosh SS;
Human adenine nucleotide translocator-2 (ANT-2) protein
                                 07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                               AAU01199;
                                                                                          AAU01199 standard;
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                                                                                                                                                                                                                           2000-365619/31.
)B; AAD00520.
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                              (first entry)
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                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1454; D
Pred. No. 1.7e
13; Mismatches
                                                                                          298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             produce adenine nuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
1.7e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translocator
                                                                                                                                                                  296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Szabo TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Disclosure; Fig

2; 186pp; English

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Human; adenine nucleotide translocator-2; ANT-2; MTP; cycloph mitochondrial permeability transition pore component; cell su mitochondrial core component; mitochondrial related disorder;
                                                                                                                                                                                                     New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polypucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                               N-PSDB; AAS05902
                                                                                                                                                                                                                                                                        Murphy AN,
Velicelebi
                                                                                                                                                                                                                                                                                                                 03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                   03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                    10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease;
                                                                                                                                                                                                                                                                                                 (MITO-) MITOKOR.
                                                                                                                                                                                                                                                        2001-291054/30
                                                                                                                                                                                                                                                                                Clevenger
                                                                                                                                                                                                                                                                                                                                   2000WO-US30535
                                                                                                                                                                                                                                                                                                                  99US-0434354
                                                                                                                                                                                                                                                                                                                                                                                                     diabetes
                                                                                                                                                                                                                                                                        RE;
                                                                                                                                                                                                                                                                                Wiley
                                                                                                                                                                                                                                                                                                                                                                                                     mellitus;
                                                                                                                                                                                                                                                                                SE,
                                                                                                                                                                                                                                                                                Andreyev
                                                                                                                                                                                                                                                                                                                                                                                                     hyperproliferative disorder
                                                                                                                                                                                                                                                                                ΑY,
                                                                                                                                                                                                                                                                                Frigeri LG
                                                                                                                                                                                                                                                                                                                                                                                                                     cell survival;
                                                                                                                                                                                                                                                                                                                                                                                                                              cyclophilin;
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(e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating tropic of ADP across the mitochondrial inner membrane. ANT proteins hyperproliterative present sequence disorders e.g. cancer, represents human adenine nucleotide tra proteins are mitochondrial permeability and deafness. translocator-2 interact

Sequence 298 Ą,

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Best Local :
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181
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                                                                                                                                                                 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
            VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                               GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                   MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                  IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                94.2%;
                                                                                                                                                                                                        13;
                                                                                                                                                                                                                   Score 1454;
Pred. No. 1
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                   DB 22;
1.7e-147;
                                                                                                                                                                                                                               Length
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AAU10379
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                                                                                                                                                                                                      comprising a regulated promoter operably linked to a nucleic acid concoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant and culturing the host cell. (I) is also useful for targeting a polypeptide cell and culturing the host cell. (I) is also useful for targeting a polypeptide of culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is cexpressed as a fusion protein with the polypeptide of interest. (C expressed as a fusion protein with the polypeptide of interest. (C cuseful for identifying an agent that binds to an ANT polypeptide. ANT cuseful for determining the presence of an ANT polypeptide. (C preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The presence of the ANT polypeptide covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide.
                                                                                                                      Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant expression construct (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenine nucleotide translocator 2 (ANT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10379 standard; Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055598/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2002 (first entry)
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IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenine nucleotide translocator; ANT; ss;
                                                                                                                                    Similarity
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                                                                                                                    Conservative
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                                                                                                                                  94.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clevenger W, W Y, Carroll AK;
                                                                                                                                  Score 1454; DB 23; Pred. No. 1.7e-147;
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                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for producing adenine nucleotide regulated promoter linked to -
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                                                                                                                                               Length
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                                                                                                                    Gaps
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RESULT 9
AAW61169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                             metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These mode systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane
                                                                                                                            The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl CDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative
                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-286608/25
N-PSDB; AAV36479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9819714-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti, Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OxpHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ant1 protein
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Sequence
                                                                                                                                                                                                                                                                                 Disclosure; Page 39-40; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graham BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lactic acidosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGIIIYRAAYEGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
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                                                                                                                                                                                                                                                                                                                  therapies
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 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMORY
   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative muscle disease.
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Query Match Best Local Similarity

91 . 5%;

Score Pred.

1412; No. 5.

DB 19; .6e-143;

Length

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ARESULT 10
ARAY71031
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AC AAY71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dyst diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                  The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of
                                                                                                                                                                                                                                                                                                                                               03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial
                                                                                                                            polypeptide, useful e. against mitochondrial
                                                                                                                                                                                                                                                          Ghosh
                                                                                                                                                                                                                                                                       Anderson CM,
                                                                                                                                                                                                                                                                                                                                                                                                   03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200026370-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiParkinsonian;
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                                                                                                                                                                Recombinant
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DB; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYEGYYDTAKGMLPDPKNTHIVVSWMIAQTYTAVAGVVSYPEDTVRRRMMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator ANT1.
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                                                                                          Page
                                                                                                                                           construct encoding adenine nucleotide translocator useful e.g. in screening for potential therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e nucleotide translocator; ANT1; mitochondria; ADP; ATP; phosphate; adenosine tri.phosphate; apoptosis; MPT; cancer; permeability transition; neuroprotective; nootropic; lan; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
                                                                                                                                                                                                                                                                         Davis
                                                                                                                                                                                                                                                                                                                                               98US-0185904
99US-0393441
                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25883
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                                                                                                                                                                                                                                                                         RE,
                                                                                                                            .g. in screening disease
                                                                                                                                                                                                                                                                         Clevenger
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                                                                                          English
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   transport
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   of adenosine
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   N-PSDB; AAS05901
                                                  Murphy AN, C. Velicelebi G,
                                                                                                                                                                                                                    10-MAY-2001.
                    WPI; 2001-291054/30
                                                                                                                                             03-NOV-1999;
                                                                                                                                                                                 03-NOV-2000; 2000WO-US30535
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                                                                                                         (MITO-) MITOKOR
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Query Match
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                                                                                                                                                                                             VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIEVSWMIAQSVTAVAGLLSYPEDTVRRRMM
                                                                                                                                                                                                                                           VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
     QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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87.2%;
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Pred. No. 3.96
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Mismatches 16;
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mitochondrial permeability transition pore component; cell su mitochondrial core component; mitochondrial related disorder; Alzheimer's disease; diabetes mellitus; hyperproliferative di
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WO200132876-A2
                                                                                                                                                                                                                   Human adenine nucleotide translocator-1 (ANT-1) protein
                                                                                                                                                                                                                                                                                                                                                                 AAU01198
                                               sapiens
                                                                                                                                                                      adenine
                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                    nucleotide translocator-1; ANT-1;
                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                   297
                                                                                                                                                                    MTP; cyclophilin;
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disorder survival;

Clevenger

99US-0434354

Davis

RE;

Wiley

SE,

Andreyev

ΑÝ,

Frigeri

<u>ن</u>

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RESULT 12
AAU10378
ID AAU10
XX
AAU10378
AC AAU10
XX
AC AAU10
XX
II 4-FE
XX
Humar
XX
Humar
XW
Humar
XW
Humar
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Homo
XX
OS Homo
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PD 15-N
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Best Local S
Matches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability translition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MT and/or cell survival. These agents are useful for the prevention treatment of diseases associated with altered mitochondrial function dysfunctional cell survival, such as Alzhelmer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents human adenine nucleotide translocate (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid
 15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                      mitochondrial
                                                                                                                  Human; adenine
                                                                                                                                                       Human
                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                          AAU10378;
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                                   WO200185944-A2
                                                                    Homo
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                                                                                                                                                       adenine
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                                                                                                                                                                                       (first entry)
                                                                                                  matrix protein
                                                                                                                                                       nucleotide translocator 1 (ANT1).
                                                                                                                      nucleotide translocator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186pp; English.
                                                                                                                                                                                                                                                            Protein;
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Pred. No. 3.9e-140;
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RESULT 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for trageting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                          ABG15423 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for identifying an agent that interacts with an ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant expression construct
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                                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                      OSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                      MGDHAWSFLKDFLAGAVAAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-055598/07.
                                                                                                                                                                                                                                                                  VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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                                                                                          Protein;
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Pei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 1385.5; DB 2
87.2%; Pred. No. 3.9e-140;
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Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for producing adenine nucleotide regulated promoter linked to
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human ANT1.
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18-FEB-2002

(first entry)

diagnostic protein #15414.

ABG15423

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CC Note: The sequence data for this patent did not appear in the printed CC affection, but was obtained in electronic format directly from WIPO cat from wino introub. Outpublished not sequences.
 В
                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20;
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                                                                                                                                                                                                                                                                                                                                                      Sequence
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   204
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                                                                                                                                                                                                                             1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                         IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      supplement;
                  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTV-TAVAGVVSYPFDT--VRRR 237
                                                                                                                                                                                                           MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIIGCVVR
GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                       IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFARNLASG
                                                                                                                                                                                                                                                                                    263;
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                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US08631
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medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                               88.6%;
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                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                            Score 1367.5; DB 22
Pred. No. 3.8e-138;
3; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                                                                 Length
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1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR

Query Match Best Local Matches

Local Sin

Similarity

83.5%;

Score 1288; Pred. No. 9.

; DB 22; 9.6e-130; nes 7;

Conservative

12;

Mismatches

Indels Length

0,

Gaps

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (R) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or cquantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG0377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO at them wino int/nnh/nnh/ished pot sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome food supplement;
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 57415; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
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                              ftp.wipo.int/pub/published_pct_sequences.
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 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic protein #27047
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2000US-0649167
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maging; diagnostic;
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RESULT 15
ABB66082
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Best Loc
Matches
                                               Query Match
                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL101640-ABL16175) and the encoded proteins (ABB1737-ABB72072).
                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic agenes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
N-PSDB; ABL10185.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 25038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
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Search completed: November 12, 2002, 16:45:58 Job time: 31.0336 secs

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Query Match 91.5%; Sco Best Local Similarity 88.6%; Pro Matches 264; Conservative 19;	US-08-961-871-10 US-08-961-871-10 US-08-961-871-10 Sequence 10, Application US/089618; Patent No. 6013858 GENERAL INFORMATION: APPLICANT: Wallace, Douglas C. APPLICANT: Graham, Brett H. APPLICANT: MacGregor, Grant R. TITLE OF INVENTION: Mouse Lack TITLE OF INVENTION: Mucleotide CORRESPONDENCE ADDRESS: APPLICATE: SJ70 Manhattan Circle CITY: Boulder STREET: SJ70 Manhattan Circle CITY: Boulder STREET: Greenlee, Winner a STREET: SJ70 Manhattan Circle COUNTRY: US ZIP: 80303 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-1 SOFTWARE: Patentin Release # CURRENT APPLICATION NUMBER: US/08/96. FILING DATE: J1-OCT-1997 CLASSIFICATION NUMBER: US/08/96. FILING DATE: J1-OCT-1997 CLASSIFICATION NUMBER: US 60/03. FILING DATE: J1-OCT-1997 CLASSIFICATION NUMBER: US 60/03. FILING DATE: J1-OCT-1997 CLASSIFICATION NUMBER: J8-07-1996 ATTORNEY/AGENT INFORMATION: NAME: Fetber, Donna M. REGISTRATION NUMBER: J8-07-1996 ATTORNEY/AGENT INFORMATION: NAME: Fetber, Donna M. REGISTRATION UNMBER: J8-07-1996 ATTORNEY/AGENT INFORMATION: TELEPHONE: J030 499-8080	28 226.5 14.7 303 2 US-0 29 226.5 14.7 303 2 US-0 30 226.5 14.7 303 3 US-0 31 226.5 14.7 303 3 US-0 31 226.5 14.4 293 4 US-0 32 222 14.4 293 4 US-0 34 205.5 13.3 307 3 US-0 35 205.5 13.3 307 3 US-0 36 205.5 13.3 307 3 US-0 37 198.5 12.9 351 4 US-0 40 191 12.4 256 2 US-0 41 191 12.4 256 2 US-0 42 191 12.4 256 3 US-0 43 191 12.4 256 3 US-0 44 180.5 11.7 312 4 US-0 45 180.5 11.7 312 4 US-0
91.5%; 88.6%; vative 19	ication US/08961871 8 811ace, Douglas C. raham, Brett H. 2012 Mouse Lacking Heart-Muscle Adenine MTION: Mucleotide Translocator Protein and Methods JENCES: 1 Greenlee, Winner and Sullivan, P.C. Manhattan Circle, Suite 201 Per STEM: PC DOS/MS-DOS Patentin Release #1.0, Version #1.30 AATION DATA: NUMBER: US/08/961,871 31-OCT-1997 TON: 800 TION DATA: NUMBER: 33,878 NUMBER: 33,878 NUMBER: 33,878 NUMBER: 33,978 NUMBER: 33,978 NUMBER: 78-96 TION INFORMATION: G. 101 NO: 10: G. 201 49-8080 303) 49-8089 SEQ ID NO: 10: G. 201 10: G. 201 10: G. 201 10: G. 201 201 201 G. 201 201 G. 201 201 G. 201	

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Atthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
RESULT 3
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
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Best Local Similarity
Matches 88; Conserv
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TYPE: PRT
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                                                                                                                                                                                                                              AYFGVYDTAKGMLPDPKNTHI-------VVSWMIAQTVTAVAG-VVSYPFDTVRRR 237
                                                                                                                                                                                                                                                                                                    FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA
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ilarity 29.4%; Pred. No. 1.3e-26;
Conservative 62; Mismatches 111;
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; SOFTWARE: FastSE; SEQ ID NO 2; LENGTH: 291; TYPE: PRT; ORGANISM: Homo sUS-09-501-558-2
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Query Match
Best Local S
Matches 80
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                                                                                                                                       SEQ ID NO 4
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CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                   APPLICANT: KRIEF, STEPHANE APPLICANT: SOUCHET, MICHEL APPLICANT: BRIL, ANTOINE
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                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30985
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                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
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                                                                                     ORGANISM: HOMO
                                                                                                      TYPE: PRT
                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMQSG-RKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIVVGVELPVYDITKKHLILSGLMGDTVYTHFLSSF----TCGLAGALASNPVDVVRTRM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGLKALYSGIAPAMLRQASYGTIKIGTYQSLKRLFIERPEDET-----LPINVICGILSG 117
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87; Conserv
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80;
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Sands, Arthur T.
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Mathur, Brian
Conservative
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28.9%;
                18.1%;
27.1%;
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; Pred. No. 8.3e-24;
54; Mismatches 129;
47;
                Score 280; DB 4;
Pred. No. 3.9e-23;
 Mismatches
                                  Length 447;
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; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO S
US-09-160-119-2
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RESULT 6
US-09-142-565-2
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Best Local Similarity
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APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH 30985
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                                                                                                                                                                                                                                                                                                                                                                                  323 OVAESAYRFGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 YEGFFGLYRGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP------LAAEILAG
                                                                        547 LQVAARAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYEL
                                                                                                                                                                                                                                                                                                        383 YEGFFGLYRGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP------LAAEILAG
                                                                                                              240 MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEL 294
                                                                                                                                                  489 FLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTR--
                                                                                                                                                                                                                                                                  121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
                                                                                                                                                                                                                                                                                                                                            EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKHTQFWRYFAGNLASG 120
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                                                                                                                                                                                                                            GCAGGSQVIFTNPLEIVKIRLQV-AGEITTGPRVSAL----SVVRDLGFFGIYKGAKAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 280; DB 4; Length 674; Pred. No. 7.3e-23; 7; Mismatches 148; Indels
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                                                                          601
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Best Local Similarity
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EARLIER FILING DATE: 197-07-16
NUMBER OF SEO ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version :
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
                                                                                                                                                                                                                                                                                                                  Sequence 56, Application US/08518878B Patent No. 5702902
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FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Tartag
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                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                          STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL-GGVDKHTQFWRYFAGNLASGGAA 123
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                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ--HASKQIAADKQYKGIVDCIVRIPKE 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGPCSPYNGLVAGLQRQMSFASIRIGLYDSVKQVYTPKGADNSSLTTRILA-----GCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RAL 301
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                                                                                                                                     New York
                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLK 298
                                                                                                                                                                                                                                      TREATMENT
                                                                                                                                                                                                                                      COMPOSITIONS
TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.2%; Score 265; DB 4; 27.1%; Pred. No. 1.1e-21; tive 52; Mismatches 145;
                                                                                                                                                                                                                                      AND METHODS
BODY WEIGHT
                                                                                                                                                                                                                                      FOR THE DISORDERS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
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                                                                                                                                                                                                                                        INCLUDING OBESITY
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RESULT 8
US-08-470-868A-56
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GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAURA A.
REGISTRATION UMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06-JUN-19
CLASSIFICATION: 530
                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
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                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036
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STRANDEDNESS: sir
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 23-AU
NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAYEGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
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                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                       New York
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1155 Avenue of the Americas
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                                                                                                              PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 790-9090
                                                                                                                                                                          Floppy disk
                                                     06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1995
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24.9%; Pred. No. 4.7
                                                                         US/08/470,868A
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US-08-518-878B-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08518878B Patent No. 5702902 GENERAL INFORMATION:
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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LENGTH: 299 amino acids
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TELEPHONE: (212) 790-9090
                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
     TELEFAX: (211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 -- NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
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                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
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                                                                                                            REGISTRATION NUMBER:
                                                                                                                                 NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                            Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                         New York
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                                    (212) 869-9741/8864
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS,
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                                                                                                  30,742
FR: 78
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GENERAL INFORMATION:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 309 amino acids
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                   NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 788
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                              FILING DATE: 23-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 23-AUG-
APPLICATION NUMBER:
FILING DATE: 06-JUN-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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TOPOLOGY: un
                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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FOR SEQ ID NO:
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                   66141 PENNIE
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METHODS AND COMPOSITIONS F
METHODS AND COMPOSITIONS F
METHODS AND COMPOSITIONS F
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                                                                                                                                                              UMBER: US 08/294,522
23-AUG-1994
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                                                                                                                                                                                                                                                       US 08/518,878
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of the Americas
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US-08-470-868A-51
US-08-470-868A-51
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                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 06-JUN-199
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                 TELEFAX: (¿1.,
TELEFAX: (¿1.,
METEX: 66441 PENNIE
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                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
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                TOPOLOGY:
                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                    10036
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74; Conservative
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                                                                                                                                    (212) 869-8864
              unknown
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                                                                 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
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Treatment of Body Weight
                                                                                                                                                                                                                                                                                                                               Release #1.0,
                                                                                                                                                                                                                                                                                            US/08/470,868A
                                                                                                                                                                                                  30,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Including Obesity
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US-09-210-681-51

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US-09-210-681-51; Sequence 51, A
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                                                                TELEPHONE: (212) 790-90:
TELEFAX: (212) 869-9741.
TELEFAX: (211) BOUNTE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                          NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
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STRANDEDNESS:
TOPOLOGY: un
                                   TYPE:
                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                        FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/518,878 FILING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                    LENGTH:
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                                 amino acid
                                                 309 amino acids
                                                                                                                        (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATION: LOUIS A.
TRATTAGLIA, LOUIS A.
VENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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24.9%; Pred. No. 4.9
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RESULT 13
US-08-946-719A-51
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GENERAL INFORMATION:
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Best Local
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                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                          APPLICATE: 23-AUG III
FILING DATE: 23-AUG III
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
NAME: COTUZZI, Laura A.
NAME: 30,742
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US.08/807,861
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                  SEQUENCE CHARACTERISTICS:
                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 26-FEB
APPLICATION NUMBER:
FILING DATE: 23-AUG
APPLICATION NUMBER:
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                                                                                                                                                                                                          FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
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                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/
FILING DATE: 8-OCT-1997
                                                                          TELEFAX:
                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
LENGTH:
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es 74; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEWRGNLANVIRYEPTQALNEAEKDKYKQIFLGGVDKHTQEWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTTAREEGFRGLWKGTSPNVARNAIVN 190
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5. 6121017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
Y: U.S.A.
                                                                        (212)
(212) 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tartaglia, Louis A.
VENTION: COMPOSITIONS FOR THE TREATMENT AND
VENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                    23-AUG-1995
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24.9%;
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                                                                                                                                  7853-107
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Pred. No. 4.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 309;
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; TOPOLOGY: US-08-946-719A-51

STRANDEDNESS: single

unknown

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US-08-775-009-33
US-08-775-009-33
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            COUNTAL.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

COMPOTER: PC-DOS/MS-DOS

COMPOTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION UNMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-(
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical
                                                                                                                                                               TELEPHONE: (215) 568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 AAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                   TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                              FILING DATE: 27-DEC CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
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                                                                                       311 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emanuel,
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                                                                                                                                                568-3439
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24.9%; Pred. No. 4.9
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ches 146;
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Region
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                                                                  ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-937-466-4
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US-08-937-466-4
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 Query Match
Best Local Sin
Matches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5846779
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acid
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Ning APPLICANT: Amaral, M. (APPLICANT: Chen, Jin-La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 AHK----YRNTLDCGVQILKNEGPKAFYKGTVPRLGRVCLDVAIVFVIYDEVVKLL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 NQAIREFVMTSLRNWY-QGDNPNKPMNPLITGVFGAVAGAASVFGNTPLDVIKTRMQGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 YRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSY----PFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
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                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 LYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDSR------RGLLCGLGAGVAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 KAILAGGLAGGIEICITFPTEYVKTQLQLD----ERANPPRYRGIGDCVRQTVRSHGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVVVVCPMETVKVKFIHD -- QTSSNPKYRGFFHGVREIVREQGLKGTYQGLTATVLKQGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIII 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWRGNLANVIRYFPTQALNFA----FKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94010
Similarity 26.8
79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HILLSBOROUGH
                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amaral, M. Cat
Chen, Jin-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                        (650) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                  s: single
linear
                                                                                                                                                                                                                        (650)
                                                                                                                                                   amino acids
                                                                                    peptide
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                 15.9%;
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                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                          US/08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catherine
                                                                                                                                                                                        4..
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 50;
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Pred. No. 4.9e-20;
3; Mismatches 135;
                                                                                                                                                                                                                                                         T97-009
               Score 245; DB 2;
Pred. No. 3.4e-19;
   Mismatches
   144;
                                 Length 432;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 311;
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   22;
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Search completed: November 12, 2002, 16:49:20 Job time: 13.0131~secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          າ DB seq
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Published_Applications_Aa:*

1: /cgn2_6/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/ptodata/1/pubpaa/
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1543
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                                                                                                                                                /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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     /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

18 19	16 17	154	13	12	10	9	8	7	6	₅	4	ω	2	مبر	Result No.
314 314	314 314	314	333.5	368	423	518	749.5	760.5	1385.5	1385.5	1454	1454	1543	1543	Score
20.3	20.3 20.3	20.3	21.6	23.8	27.4	33.6	48.6	49.3	89.8	89.8	94.2	94.2	100.0	100.0	Query Match Length
469 469	469 9	469	410	477	175	132	386	318	297	297	298	298	298	298	Length [
10 10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
US-09-989-727-289 US-09-989-731-289	US-09-989-723-289 US-09-989-279-289	US-09-989-722-289	US-09-777-921A-5	US-09-777-921A-2	US-09-864-761-36440	US-09-925-301-1459	US-09-734-569-170	US-09-801-368-252	US-09-810-644-31	US-09-811-094-31	US-09-810-644-32	US-09-811-094-32	US-09-810-644-33	US-09-811-094-33	ID
	Sequence 289, App Sequence 289, App	Sequence 289, App Sequence 289, App	Sequence 5, Appli	Sequence 4, Appli Sequence 2, Appli		Sequence 1459, Ap		Sequence 252, App	Sequence 31, Appl	Sequence 31, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 33, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	t
218	222.5	232.5	240.5	241.5	242	246.5	250	250.5	254.5	257	257.5	264	265	265	265	274.5	309	314	314	314	314	314	314	314	
14.1	14.4	15.1	15.6	15.7	15.7	16.0	16.2	16.2	16.5	16.7	16.7	17.1	17.2	17.2	17.2	17.8	20.0	20.3	20.3	20.3	20.3	20.3	20.3	20.3	
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US-09-796-766-14	US-09-810-673A-6	US-09-840-787-12	US-09-796-766-21	US-09-808-457-4	US-09-796-766-10	US-10-006-867-126	US-09-796-766-18	US-09-884-814-6	US-09-884-814-1	US-09-925-300-1808	US-09-884-814-8	US-10-042-194-1	US-09-808-457-2	US-09-826-507-2	US-09-734-134-2	US-09-796-766-20	US-09-777-921A-6	US-10-006-867-58	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	00 00 000
14,	Sequence 6, A	Sequence 12,	Sequence 21,	Sequence 4, A	Sequence 10,	Sequence 126,	Sequence 18,	Sequence 6, A	Sequence 1, Appli	Sequence 1808	Sequence 8, Appl	Sequence 1, Appli	Sequence 2, A	•	Sequence 2, A	20	Sequence 6, A	Sequence 58,	Sequence 289,	nedactice vol.					
Appl	Appli	Appl	Appl	Appli	Appl	126, App	App1	Appli	\ppli	³, Ap	\ppli	ilqc	Appli	Appli	Appli	App1	Appli	7	App	App	App	App	App	App	240

ALIGNMENTS

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RESULT 1
US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo sapien US-09-811-094-33
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
                                                                                                                                                                                                   Query Match 100.0%; S
Best Local Similarity 100.0%; F
Matches 298; Conservative 0;
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Chris
APPLICANT: Davis, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                   1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pel, Yazhong
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Christen M
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Pred. No. 3.8e-152;
); Mismatches 0;
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Sequence 32, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
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Best Local S
Matches 298
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SEQ ID NO 33
LENCTH: 298
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
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CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 1543; DB 10; Local Similarity 100.0%; Pred. No. 3.8e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
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                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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Clevenger, William Wiley, Sandra Eileen Willer, Scott W. Szabo, Tomas R.
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Clevenger, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-810-644-32
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                                                                        US-09-810-644-32
                                                                                                   CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Soott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 32
LENGTH: 298
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                Query Match
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                             TITLE OF INVENTION: PRODUCTION OF ADENINE ITITLE OF INVENTION: NOVEL ANT LIGANDS AND FILE REFERENCE: 660088.420D3
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                                                                                     ORGANISM: Homo sapien
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Local Similarity 92.6%; Pred. No. 6.1e-143;
Comparison 13; Mismatches 9;
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   274;
                  Similarity
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Moos, Walter H.
Pei, Yazhong
   Conservative
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                  94.2%;
92.6%;
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   13;
Score 1454; DB 10;
Pred. No. 6.1e-143;
3; Mismatches 9;
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APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
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CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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                                              GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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US20010044144A1
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pred. No. 7.46
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APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
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ORGANISM: Homo
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Szabo, Tomas R.
Ghosh, Soumitra S.
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Milne, Todd
No. US20020128250Alman,
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Pei, Yazhong
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Salama, Sofie
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Madden, Kevin
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Pred. No. 7.4e
21; Mismatches
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APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, The
APPLICANT: Reindl, Andreas
APPLICANT: Cirpus, Petra
                         Query Match
Best Local Similarity
Matches 157; Conserv
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Best Local Similarity
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PRIOR ETLING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR ETLING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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EQ ID NO 252
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 181
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16
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CURRENT FILING DATE: 2001-05-24
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                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRIPKEQ
   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLCFVYPLDFARTRLAAD--VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKEEGYAKWFAGNLASGGAAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS
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SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRIPKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQMIL
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                                                                                                                                                                                                                                                                                                                                               Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cirpus, Petra
Bischoff, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                    Frank, Markus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renz, Andreas
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Pred. No. 3.1
                                Score 749.5; DB 10;
Pred. No. 6.7e-70;
4; Mismatches 84;
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SEQ ID NO 1459
LENGTH: 132
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APPLICANT: Rosen et al.
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Sequence 36440, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                   Matches 103;
                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally
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LOCATION: (129)
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LOCATION: (126)
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLCFVYPLDFARTRLAADV----GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLLFVYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGTAGLYRGFAISCA
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                                                                                                                                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 85
                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFXFKDKYKQXFLXGVXKHT
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                                                                                                                                                                                                                                   Score 518; DB 10; Pred. No. 1.4e-46;
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GENERAL

INFORMATION

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Best Local
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 36440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROAFRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
TYPE: PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLYKITKSDGIRG 172
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
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Chen, Wensheng
                                                                   Conservative
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EST_HUMAN
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                                                                                                                                                                                                                                    EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
EXPRESSED IN BONE MARROW, SIGNAL = 1.9
EXPRESSED IN PLACENTA, SIGNAL = 2.2
EXPRESSED IN HEART, SIGNAL = 7.3
EXPRESSED IN HELA, SIGNAL = 7.7
EXPRESSED IN BT474, SIGNAL = 2.7
                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED IN LUNG, S. EXPRESSED IN HBL100,
                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP TO L78810.1
                                                                                   27.48;
93.18;
                                                                                                                                                                         IN BRAIN, SIGNAL = 2
HIT: P05141, EVALUE 6.00e-38
HIT: AW935235.1, EVALUE 5.30e-37
                                                               Score 423; DB 10;
Pred. No. 5.4e-37;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                     LUNG, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                            IGNAL = 3.2
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                                                                                                        Length 87;
                                                                 Indels
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US-09-777-921A-4
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                                     ; ORGANISM: Homo sapiens US-09-777-921A-2
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US-09-777-921A-2
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TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4
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SEQ ID NO 4
                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09777921A Patent No. US20020115136A1
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Query Match
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TITLE OF INVENTION: ISCATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/777,921A CURRENT FILING DATE: 2002-02-07
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                                                                              TYPE: PRT
                                                                                                 LENGTH: 477
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Pred. No. 2.6e-30;
  Score 368;
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US-09-777-921A-5
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                                                                                                                                        RESULT
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Patent NO. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
                                                       Sequence 289, Application US/09992598 Patent No. US20020160384A1 GENERAL INFORMATION:
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Matches
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Best Local :
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LENGTH: 410
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APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
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SOFTWARE: FastSEQ for
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Pred. No. 7.9e
45; Mismatches
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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OR FILING DATE: 1997-11-13
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OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
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OR FILING DATE: 1998-06-02
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OR APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-05-07
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Stewart, Timothy A.
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Kljavin, Ivar J
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/090676
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-24
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FILING DATE: 1998-07-02
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OR APPLICATION NUMBER: 60/089947
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R APPLICATION NUMBER: 60/090355
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60/089600 60/089599

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FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876

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CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C63
                                                                                                                                                                                                      DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR FILING DATE: 1998-05-07

DR APPLICATION NUMBER: 60/084600

DR FILING DATE: 1998-05-28

DR APPLICATION NUMBER: 60/087607

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DR APPLICATION NUMBER: 60/087759

DR FILING DATE: 1998-06-02

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OR FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08
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Godowski, Paul
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Botstein, David
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J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03894
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A;Molecule type: mRNA
A;Residues: 36-104',R',106,'A',109-298 <HOU>
A;Cross-references: GB:J03592; NID:g339722;
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
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A; Residues: 1-298 <COZ>
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
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              GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                                                                                                                      Score 1543; DB 1;
Pred. No. 6.6e-129;
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A;Accession: A;Accession: A;Accession: A;Accession: A;Rolecule type: mRNA A;Molecule type: mRNA A;Residues: 1-298 <BAT>
A;Residues: 1-298 <BAT>
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; R;Houldsworth, J.; Attardi, G.
R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
                                                                                                                                                                                                                       ADP,ATP carrier protein T2 - human
N;Alternate names: mitochondrial ADP,ATP translocase 2
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change
C;Accession: A29132; C28116
R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-298 <POW>
A; Residues: 1-298 <POW>
A; Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
A; Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
C; Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology <ACP1>
F; 5-99/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F; 207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
B43646
ADP,ATP carrier protein T2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
C:Accession: B43646
                                                                                                                                                             J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a
A;Reference number: A29132; MUID:87166056;
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A;Title: Two bovine genes for mitochondrial ADP/ATP translocase A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
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A; Residues: 1-298 < PO
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97.7%;
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                                                                                                                                                                human ADP/ATP
PMID:3031073
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C; Accession: I60173
R; Shinohara, Y.; Kamida, M.; Yamazaki, N.; R; Shinohara, Y.; Kamida, M.; Yamazaki, N.; R; Shinohara, Y.; Kamida, M.; Yamazaki, N.; R; Shinohara, Y.; Kamida, M.; Yamazaki, N.; Ramazaki, N.; Ramazaki, N.; Yamazaki, N.; Ramazaki, N.; Yamazaki, Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamazaki, N.; Yamaz
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A; Molecule type: mRNA
A; Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A; Cross-references: GB.J03591; NID:g339720; PIDN:AAA36749.1;
A:Francimental source: clone pHAT3
                                                                                                                                             F;5-99/Domain: ADP
F;110-202/Domain:
F;207-298/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenine nucleotide translocator -
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F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Residues: 1-298 <R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
                                                                                                                                  Fintrons: 37/3; 200/1; 247/1; Superfamily: ADP,ATP carrier protein is Superfamily: ADP,ATP carrier protein protein it Reywords: duplication; transmembrane protein repeat homology <ACP1>;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NID: g400426; PIDN: CAA43842.1;
                                 Score 1424;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1454;
Pred. No. 4
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                                     .2e-118;
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MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR

F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental F;52/Modified site: N6-methyllysine (Lys) #status predicted

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A:Cross references: GB:M24102: NID:g529414; PIDN:AAA30768.1; PIDR:ACTOSS references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PIDR:RABSMUSSEN, U.B.; WOhlrab, H.

Blochem. Blophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinterest of the commun. 138, A:Residues: 208-298 cARS-A:AS-A:Residues: 208-298 cARS-A:AS-A:Residues: 208-298 cARS-A:AS-A:Residues: 208-298 cARS-A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1: PIDR:AAA30363.1: P
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N;Alternate names: ADP/ATP translocase T1

C;Species: Bos primigenius taurus (cattle)

C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change

C;Accession: A43646; A24822; A03181; A61343; S69369

R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808

A;Rocession: A43646

A;Molecule type: mRNA
A;Residues: 1-298 < POW>
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    ;Description: catalyzes the exchange between cytosolic ADP and ;Note: located in the inner mitochondrial membrane ;Superfamily: ADP,ATP carrier protein; ADP ATP carrier protein; Keywords: acetylated amino end; duplication; homodimer; methyl; S-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>;110-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>;207-298/Domain: ADP,ATP carrier protein rep
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N;Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Av
C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37210
A;Accession: S37210
A;Accession: S37210
A;Accession: S37210
A;Accession: S37210
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <LAP>
A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g-
C;Genetics:
A;Gene: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Superfamily: ADP,ATP carrier protein repeat homology <ACP1>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                       GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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Pred. No. 3
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Pred. No. 7
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Mismatches
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.6e-118;
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A;Map position: 4435-4435
A;Map position: 4435-4435
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protei
F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Residues: 1-15, 'A; 17-146, 'RR', 149, 151-226, 'L', 228-298 <
A; Residues: 1-15, 'A; 17-146, 'RR', 149, 151-226, 'L', 228-298 <
A; Cross-references: GB:J02966; NID:9339919; PIDN:AAA61223.
A; Experimental source: clone pHMANT
R; Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A; Title: Two distinct genes for ADP/ATP translocase are ex
A; Reference number: A94197; MUID:88124845; PMID:2829183
A; Accession: A28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-298 < COZ>
A; Residues: 1-298 < COZ>
R; Neckelmann, N; Li, K; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A; Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader A; Reference number: A39891; MUID:88041149; PMID:2823266
A; Accession: A39891
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A; Title: A human muscle adenine nucleotide translocator A; Reference number: A44778; MUID:89340499; PMID:2547778
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C; Date: 17-Mar-2000 #sequence
C; Accession: A44778; S03893;
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A44778

ADP,ATP carrier protein T1 - human
ADP,ATP carrier initochondrial ADP,ATP translocase
N;Alternate names: mitochondrial ADP,ATP translocase
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A; Residues: 1-37 <HOU>
A; Cross-references: GB:J03593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_ci
C;Accession: A44778; S03893; A39891; A28116
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh,
                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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A; Residues: 1-298 <L
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rocal Similarity
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                                                      GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                        IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                              MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                            GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                                               IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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88.3%;
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A39891; A28116
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                                                                                                                                                                                                                                                                                                                                                      Score 1409; DB 1;
Pred. No. 4.7e-117;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                 16;
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A:Molecule type: DNA
A:Residues: 1-301 <BEA>
A:Residues: 1-301 <BEA>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Superfamily: ADP,ATP carrier protein
C:Keywords: duplication; transmembrane protein
C:Keywords: duplication; transmembrane protein
                                                                                                                                                                                                                       R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier
                                                                                                                                                                                                                                                                                                  ADP.ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936
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C;Species: Mus musculus (house mouse)
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                                                                                                                                                                                                  A; Reference number: S31935
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Best Local :
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89.2%;
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Pred. No. 1.
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#text_change 10-Sep-1999

the

mosquito

Anopheles gambiae

repeat homology

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F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
                                                                                                                                                                          181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLWQVQTNDRTITADKQYKGIIDCVVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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QSGRKGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLVSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                                    IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 2;
1.1e-116;
hes 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 298;
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   296
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-313 <WIL>
A; Cross-references: EMBL: Z68218; PIDN:CAA92472.1; GSI
A; Experimental source: clone KO1H12
C;Genetics:
A;Gene: CESP: KO1H12.2
A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein K01H12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T23207 R;McMurray, A.
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                               8 FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS
            ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                       RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG
                                                                                                                       LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                     AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                     FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMQSWPCKSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVKALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
-DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                                                                                                                                                                                                                                                                                         4/1; 191/2
11y: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
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77.08;
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                                                                                                                                                                                                                                                                                                                           Score 1041; DB 2;
Pred. No. 1.8e-84;
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                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                        Length 313;
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RESULT 12
T25371
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T25850
                                                                                                                                                                                                                                                                                hypothetical protein T27E9.1 · Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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A;Molecule type: DNA
A;Residues: 1-313 <GEI>
A; Introns: 20/1; 41/3; C; Superfamily: ADP, ATP
                                                     C;Genetics:
A;Gene: CESP:T27E9.1
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-300 <WIL>
                                                                                                                                                                                                         submitted to the EMBL Data Library, A;Reference number: Z20024
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                                                                                          A; Experimental source:
                                                                                                                A; Cross-references:
                                                                                                                                                                   A; Status: preliminary;
                                                                                                                                                                                     A; Accession: T25371
                                                                                                                                                                                                                                                R; Lloyd, C
                                                                                                                                                                                                                                                                C; Accession: T25371
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                                   A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAAYEGMEDTAKMVETADGKKLNEFAANAIAQVVTVGSGILSYPWDTVRRRMMMQSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                            EMBL: Z82059; PIDN: CAB04874.1; ce: clone T27E9
115/2
carrier protein;
                                                                                                                                                                       translated
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Pred. No. 2.7e-84;
9; Mismatches 52
                                                                                                                                                                       from
                                                                                                                                                                                                                              November
                                                                                                                                                                       GB/EMBL/DDBJ
ADP, ATP carrier
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                                                                                                                GSPDB:GN00021;
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protein repeat homology
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                                                                                                              CESP:T27E9.1
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Query Match

Local Similarity

67.3%; 69.2%;

Score 1038;

Pred. No.

.2e-84; DB 2;

Length 300;

Mismatches

Indels

4

Gaps

ų

Conservative

Matches

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A; Map position:
C; Superfamily: A
F; 9-103/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
T15206
T15206
Appothetical protein W02D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T15206
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                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GNA;Experimental source: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-300 <LET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: The sequence of C. elegans cosmid A; Reference number: Z18308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology; 9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
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                                             300
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                                                                                                                                                                                                                                                                                                                                                    TEQAISFAK---DFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI
                                                                                                                                                                            VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR 237
                                                                                                                                                                                                                                                                                           VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMMQSGRK--DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHL
                                                                                                                               MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKV
                                                                                                                                                          VSVQGIIIYRAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRR
                                                                                                                                                                                                                   SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
                                                                                                                                                                                                                                  SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                            ARVPKEQGY AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA
                                                                                                                                                                                                                                                                                                                                     TKEGFDYRKFLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRMMMQSGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCFVYPLDFARTRLAADIGKA-NDREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt RAAYFGMFDTAKMVFASDGQKLNFFAAWGIAQVVTVGSGILSYPWDTVRRMMMQSGRK-}
                                                                                                                                                                                                                                                                                                                                                                                              195;
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                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                        Score 993.5; DB 2;
Pred. No. 2.7e-80;
Pred. No. 2.7e-80;
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SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAAD--KQYKGIVDCIVRIPKE
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <HATP
A;Residues: 1-301 <ADP,ATP
Carrier protein; ADP,ATP
Carrier protein repeat homology <ACP1>
F;102-203/Domain: ADP,ATP
Carrier protein repeat homology <ACP2>
F;209-301/Domain: ADP,ATP
Carrier protein repeat homology <ACP3>
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A;Residues: 1-339 <HILT>
A;Residues: 1-339 <HILT>
A;Residues: 1-339 <HILT>
A;Residues: 1-339 <HILT>
A;Residues: 1-339 <HILT>
A;Residues: 1-329 / Final App. App. Carrier protein; ADP, ATP carrier protein repeat how c;Superfamily: ADP, ATP carrier protein; mitochondrion; transmembrane protein c;Keywords: duplication; homodimer; mitochondrion; transmembrane protein r;38-134/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F;144-235/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F;241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: Sb8999, c..... G. Accession: Sb8999, c.... G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accession: G. Accessi
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C;Date: 30-Jun-1992 #sequence_revision
C;Accession: A41677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 07-May-1995 #sequence_revision C;Accession: S68993; S51132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Molecular characterisation of the ADP/ATP-transporter A; Reference number: S68993; MUID:95188918; PMID:7883016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hilgarth, C.; Sauer, N.; Tanner, J. Biol. Chem. 266, 24044-24047, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIVYRGAYFGLYDTAKGVLFKDERTANFFAKWAVAQAVTAGAGVLSYPFDTVRRRLMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK--QYKGIVDCIVRIPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                     61.1%;
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Score 943; Db 2,
Pred. No. 8.1e-76;
              45;
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Qy	125	125 ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
Db	127	
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δ	244	RKG-ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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ALIGNMENTS

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SEQUENCE FROM N.A. TISSUE-Brain, Cervix, Eye, and Lung; Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. [4] SpOUENCE OF 36-298 FROM N.A. TISSUE-Liver MEDLINE-88124845; PubMed-2829183; HOULDINE-88124845; PubMed-2829183; HOULDINE-88124845; PubMed-2829183; HOULDINE-GOIL THE TRANSLOCASE are expressed at the mRNA level in adult human liver."; Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988)!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE!- SUBURIT: HOMODIMER!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane!- SUBCELLULAR LOCATION: Integral membrane protein mitochondrial	SEQUENCE FROM N.A. MEDLINE-89236396; PubMed-2541251; Cozens A.L., Runswick M.J., Walker J.E.; "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase."; J. Mol. Biol. 206:261-280(1989). [2] SEQUENCE FROM N.A. Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., Wargolin J.F.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	LT 1 _HUMAN ADT3_HUMAN STANDARD; PRT; 298 AA. P12236; Q96C49; O1-OCT-1989 (Rel. 12, Created) O1-NOV-1990 (Rel. 16, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3) ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3). SLC25A6 OR ANT3. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

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T 01-JUL-1993 (Rel. 26, Last sequence update)

T 16-CCT-2001 (Rel. 40, Last annotation update)

T 16-CCT-2001 (Rel. 40, Last annotation update)

E ADP_ATP carrier protein, isoform T2 (ADP/ATP translocase nucleotide translocator 3) (ANT 3).

S BOP ATP CARTIAL (BOVINE).

S BOS taurus (Bovine).

S BOS taurus (Bovine).

C Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Eutheridae; Bovinae; Bovinae; Bos.

NCB_TANID-9913;

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Powell S.J., Medd S.M., Runswick, M.J., Walker, "Two bovine genes for mitochondrial ADP/ATP tr. differences in various tissues.";
Biochemistry 28:866-873(1989).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP ANI MITOCHONDRIAL INNER MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane pro-
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-!- DOMAIN: COMPOSED OF
-!- SIMILARTTV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Inner membrane; Multigene family.
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PIR; B43646; B43646.
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InterPro; IPR001993; Mitoch_carrier.
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TO THE MITOCHONDRIAL CARRIER FAMILY.
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Pred. No. 3e-127;
4; Mismatches 3;
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2 (POTENTIAL).
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InterPro: IPR002067; Mit_carrier.
InterPro: IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSTITE: PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat;
Multigene family.
TRANSMEM 12 29 1 (POTENT
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MEDLINE-90375457; PubMed-2168878;
Mt D.-H., Kagan J., Chen S.-T., Chang C.-D.,
"The human fibroblast adenine nucleotide tran
cloning and sequence.";
J. Biol. Chem. 265:16060-16063/1990)
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Becker M., Graves T.,
Submitted (JAN-1998)
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Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,

Mazzarella R.A., Schlessinger D., Chen E.Y.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
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J. Biol Chi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88124845; PubMed=2829183;
Houldsworth J., Attardi G.;
"Two distinct genes for ADPATP translocase are level in adult human liver.";
level in adult human liver.";
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FUNCTION: CAFALYZES THE EXCHANGE OF ADD AND ATP A
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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etazoa; Chordata;
theria; Primates;
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                            Transmembrane; Transport;
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP
                                                                                                                                                                                                                                                                               ADT2_RAT
Q09073;
                                                                                                 Shinohara Y., Kamida M., Yamazaki N., Terada H.;
"Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator.";
Biochim. Biophys. Acta 1152:192-196(1993).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH
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REPEAT
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         This SWISS-PROT
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                                                                                 MITOCHONDRIAL INNER MEMBRANE.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                      inner membrane.
-!- TISSUE SPECIFICITY: PRESENT IN
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                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                Rattus norvegicus (Rat).
                          -!- SIMILARITY:
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DOMAIN: COMPOSED OF
                                                                       SUBCELLULAR LOCATION: Integral
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                          POSED OF THREE HOMOLOGOUS DOMAINS.
BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Rodentia;
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Sciurognathi; Muridae;
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                                                                       membrane protein. Mitochondrial
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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                                                        "Rapid evolution homologs.";
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Ellison J.W., Li >
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[1]
                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
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s; pr00926; MITOCARRIER.
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X., Francke U.,
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5; Mismatches
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Sciurognathi; Muridae;
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                                                                                                              Shapiro L.
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Laplace C.
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
Mitochondrion; Inner membrane; Rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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the European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                 121
                                                   61
                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                    inner membrane.
GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                  U27316; AAC52838.1; -. U10404; AAA19009.1; -. X70847; CAA50196.1; -. AF240003; AAF64471.1; -.
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                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                         Score 1445; D
Pred. No. 2.7e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is not removed. Usage by and for agreement (See http://www.isb-sib
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                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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7e-121;
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    Best Local Similarity
                            Query Match
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Q05962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinohara Y., Kamida M., Yamazaki N., Terada H.;
"Isolation and characterization of CDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator.";
Biochim. Biophys. Acta 1152:192-196(1993).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
SLC25A4 OR ANT1.
                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X61667;
EMBL; D12770;
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                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00926; MITOCARRIER PROSITE; PS00215; MITOCH_CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                              REPEAT
                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                        PF00153
                                                                                                                                                                                                                                                                                                family.
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IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                   membrane;
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89
  . 68;
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  1424; DB 1;
No. 2e-119;
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                                                                                                                                                                                                                                                                                                                   Transmembrane;
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                       Length
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                                                                                                                                                                                                                                                                                                                      Transport;
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                                                                                                                                                                                                                          Strausberg R;
Submitted (APR-2002) to the EMBL/
-i- FUNCTION: CATALYZES THE EXCHA
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P48962: 062164;
01-FEB1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANC1).
SLC25A4 OR ANT1 OR ANC1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy S.E., Chen Y.-S., Graham B.H., Walla "Expression and sequence analysis of the translocase 1 and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/c; TISS
Laplace C., Costet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903724;
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ellison J.W., Li X., Francke U., Shapiro L.J.; Rapid evolution of human pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.
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                                                                                         Inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

STMTLARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                          SUBCELLULAR LOCATION:
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01_JUL_1993 (Rel. 26, I
16-CCT-2001 (Rel. 40, I
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SEQUENCE FROM N.A. MEDLINE=89229093; Powell S.J., Medd
                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Boyinae; Bos.
                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP_ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                                                                                                                       BOVIN
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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EMBL; BC003791; AAH03791.1; -.
EMBL; BC208025; AAH26925.1; -.
MGD; MGI:1353495; Slc25a4.
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S.M., Runswick
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PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
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Aquila H., Misra D., Eulitz M., K
"Complete amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use
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SUBCELLULAR LOCATION: Integral membrane
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A24822; A24822.
A43646; A43646.
                                          PKEQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASGG
           AAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
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M24102; AAA30768.1;
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                                                                                                                                   Similarity
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 Z. Physiol.

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Res. Commun. 138:850-857(1986)
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Mitoch_carrier.
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89.2%;
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METHYLATION (I
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2 (POTENTIAL)
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Cozens A.L., Runswick M.J., Walker
"DNA sequences of two expressed nuc
ADP/ATP translocase."
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P12235;
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Strausberg
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88041149; PubMed=2823266;
Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
Neckelmann Seletal muscle ADP/ATP translocator: lack
"cDNA sequence of a human skeletal muscle ADP/ATP translocator cDNA,
of a leader peptide, divergence from a fibroblast translocator cDNA,
and coevolution with mitochondrial DNA genes.";
proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
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MEDLINE-89340499; PubMed-2547778;
Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
*A human muscle adenine nucleotide translocator gene has four e
is located on chromosome 4, and is differentially expressed.";
J. Biol. Chem. 264:13998-14004(1989).
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                                                                                                "Role of adenine nucleotide translocator 1 in Science 289:782-785(2000).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP A
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MEDLINE-20385067; PubMed-10926541;
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                        MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integra
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                                                                                                                                                                             J., Juselius J.K., Tiranti V., Kyttala A., ., Keranen J., Peltonen L., Suomalainen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
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InterPro; IPR001993; Mitoch_carrier.
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial
                                                                                                                           VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                       157640; -
                                                                                           IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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88.3%;
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/FTId-VAR_012111.

V -> M (IN PEO).

/FTId-VAR_012112.

G -> A (IN REF. 3).

KGA -> RR (IN REF. 3).

V -> L (IN REF. 3).

V -> L (IN REF. 3).
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Duno P.,
RA Dodson K., J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuxskern D.R., Pacleb J.M.,
RA Raiazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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MEDLINE=20196006; PubMed=10731132;
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Zhang Y.Q., Davi
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J. Mol. Evol. 35:44-50(1992).
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wa
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yac
A Ye J., Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Estence 287:2185-2195(2000).
C-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
MITOCHONDRIAL INNER MEMBRANE.
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InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane inner membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (BY SIMILARITY)
KATEVIYKNTLHCWATIAKQE-GPCFFKGAFSNILRGTGGAFVLVLYDEIKKVL
                                                                                                                                                                        QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                             AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE
                                                              IIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGR
                                                                                                                  ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI
                          KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                   IIYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQVVTTVAGIVSYPFDTVRRRMMMQSGR
                                                                                                      ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGI
                                                                                                                                                          QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                              AVGFVKDFAAGQVSAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $43651; AAB23114.1; -
$71762; AAB31734.3; -
$10618; CAA71628.1; -
$AE003484; AAF47957.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00926; MITOCARRI
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                    18
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266
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267
268
297
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                                                                                                                                                                                                                                                                                                                     AA;
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93
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79.38;
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                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (IN REF. 1)
8 PY (IN REF. 1)
8 PS RG (IN REF. 2)
9 PC -> TGA (IN REF. 2)
9 PC -> S (IN REF. 2)
9 PC -> S (IN REF. 2)
                                                                                                                                                                                                                                                               Score 1217.5; DB 1;
Pred. No. 4.7e-101;
4; Mismatches 34;
                                                                                                                                                                                                                                                                                                                    -> S (IN REF. 1). AA639439968F9750
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Transport.
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PEF. 3 AND /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q., Zheng L.,
X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translocator) (ANT).
Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11618; AAB04104.1; -.
EMBL; L11617; AAB04105.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gambiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94348635; PubMed=8069414;
Beard C.B., Crews-Oyen A.E., Kumar V.K.,
"A cDNA encoding an ADP/ATP carrier from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Culicoidea; Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADT_ANOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                         Mitochondrion;
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insect Mol. Biol. 3:35-40(1994)
                          121
                                                  119
 179
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                                                                                                                                        1 MTEQA--ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES THE EXCHANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane
                        VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                           MTKKADPYGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCF
                                                                                                                                                                                                                                                                                                                                   PR00926; MITOCARRIER.; 3.
                                                                                                                                                                                         Similarity
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                                                                                                                                                                                         78.0%;
77.7%;
                                                                                                                                                                                                                                                                                                                         membrane;
                                                                                                                                                                               23;
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Pred. No. 7.5e
23; Mismatches
                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                       Repeat;
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(POTENTIAL).
4CC9E17C9F8DA08B CRC64;
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                                                                                                                                                                                                                                                                                                                       Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP AND ATP
                                                                                                                                                                            DB 1;
.5e-100;
les 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins F.H.;
the mosquito Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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SEQUENCE
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J. Biol. Chem. 266:24044-24047(1991).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADD AND ATP ACROSS TH
MITOCHONDRIAL INNER MEMBRANE
-I- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a centre of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formaticing the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP, ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
                                                                                                                                                                                                                                                                                        Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                        PIR; A41677; A41677.
                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorella kessleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P31692;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                              InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hilgarth C., Sauer N., Tanner W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADT_CHLKE
                                                                                                                                                                                                                                                                             Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Glucose increases the expression of the ATP/ADP translocator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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 124
                          99
                                                 64
                                                                            39
                                                                                          6 ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK--QYKGIVDCIVRIPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane
GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG
                                      EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA 123
                                                                            MAFVKDLLAGGTAGAISKTAVAPIERVKLLLQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
                          EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLFPKYSPK-TDFWRFFVVNLASGGLA
                                                                                                                                 198;
                                                                                                                                            Similarity
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108
151
209
248
304
339
                                                                                                                                 Conservative
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168
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(POTENTIAL)
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                                                                                                                                                                                                                                                                             Transmembrane;
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01-NOV-1990 (Rel. 16, L
01-CCT-1994 (Rel. 30, L
ADP, ATP carrier protein
translocator 3) (ANT 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andre B.,
 TRANSMEM TRANSMEM
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                                                                                       InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                       SGD;
                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feldmann H., Mannhaupt G., Schwarzlose C., Vette Submitted (AUG-1994) to the EMBL/GenBank/DDBJ da -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolarov J., Kolarova N., Nelson N.; "A third ADP/ATP translocator gene in J. Biol. Chem. 265:12711-12716(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-90324269; PubMed-2165073; Kolarov J., Kolarova N., Nelson N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; A Saccharomycetales;
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01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288c
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AAC3 OR YBR085W OR YBR0753
                                                Multigene
                                                                   Mitochondrion;
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                                    TRANSMEM
                                                                                  PROSITE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content by non-profit institutions as long as its content if its and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER
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S0000289; AAC3.
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Z35954; CAA85031.1;
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family.
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                                                                 Inner membrane;
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SQS
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat.
ADP,ATP carrier protein (ADP/ATP translocass translocator) (ANT).
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SEQUENCE
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Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                               Sharpe J.A., Day A.;
"Structure, evolution and expression translocator gene from Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93204887; PubMed=8455552;
                                EMBL; X65194; CAA46311.1; PIR; S30259; S30259.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FUD44-R2
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
InterPro; IPR002067; InterPro; IPR001993;
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                                                                  non-profit institutions as long as its content id and this statement is not removed. Usage by an sequires a license agreement (See http://www.isb-an email to license@isb-sib.ch).
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TO THE MITOCHONDRIAL CARRIER FAMILY.
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Matches 157; Conser
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Q09188;
Q1-NOV-1997
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewar Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson
                                                                                                                                                                                                                                                                     ADP, ATP carrier protein translocator) (ANT). ANC1 OR SPBC530.10C.
                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
                                                                                                                 Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;
"Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                  MEDLINE-96257204; PubMed-8675018; Couzin N., Trezeguet V., Saux A.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                           MEDLINE=21848401; PubMed=11859360;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                              NCBI_TaxID=4896
                                                                                                                                                                                                                                   Schizosaccharomycetales;
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No. 2e-61;
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                                                                                                                                                                                                                                                                         PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                   EMBL; AL023634; CAA19176.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

    -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
    -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                  EMBL; Z49974; CAA90275.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                               Mitochondrion;
203
                  182
                                     143
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                                                                                                                           SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK---QYKGIVDCIVRIPK
                                               GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                                                                                     EQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAA
VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRRMMM
                 QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                 TFFFDFMMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIGECFKRTAA
                                                                           EEGVISLWRGNTANVLRYFPTQALNFAFKDKFKKMF-GYKKERDGYAKWFAGNLASGGAA
                                                                                                                                                                                                                                                                                            PF00153; mito_carr;
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Pred. No. 3.9e
50; Mismatches
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(POTENTIAL).
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8AC3D16A40F41AFC
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Title:
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Maximum Match 100%
Listing first 45 summaries
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                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                 SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebri6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle
9: sp_plant:*
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11: sp_rodent:*
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13: sp_vertebri13: sp_vertebri14: sp_unclassi15: sp_rvirus:*
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1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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esult No.	Score	Query Match	Query Match Length DB	В	ID		Description
1	1451	94.0	298	6	Q8SQH5		Q8sqh5 bos taurus
N	1422	92.2	298	σ	046373		C46373 oryctolagus
ω	1421	92.1	298	13	Q919M9	•	Q9i9m9 xenopus lae
4	1418	91.9	298	11	Q62164		Q62164 mus musculu
Ç	1409	91.3	298	13	Q9PRH1		-
0	1406	91.1	298	13	Q9PRH2		Q9prh2 rana rugosa
7	1402	90.9	298	13	Q9YIC4		Q9yic4 rana rugosa
8	1300	84.3	299	σ	Q95VX4		C95vx4 ethmostigmu
9	1259	81.6	317	13	Q91336		Q91336 rana sylvat
10	1254.5	81.3	299	ഗ	Q95S30		C95s30 drosophila
11	1235.5	80.1	300	5	Q9NHW5		C9nhw5 lucilia cup
12	1187.5	77.0	288	ഗ	044093		C44093 drosophila
13	1183.5	76.7	288	ъ	044094		C44094 drosophila
14	1176.5	76.2	304	տ	Q25129		C25129 halocynthia
15	1137.5	73.7	307	G	062526		C62526 drosophila
16	1119	72.5	315	4	Q9н0С2		C9h0c2 homo sapien

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ALIGNMENTS

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121 GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLLYKITKSDGIRGLYOGFSYS 180 	61 IPKEQGYLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGYDKHTQFWRYEAGNLASG 120 	MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 : : : : : : MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60	94.0%; Score 1451; DB 6; Length 298; Similarity 92.2%; Pred. No. 5e-119; 3: Conservative 13: Mismatches 10: Indels 0:	EMBL; AB065433; BAB84673.1; SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;	Mitochondrion 1:371-379(2002).	differences in its isoforms."	identification of possible amino acids that determine functional	Yamazaki N., Shinohara Y., Tanida K., Terada H.;	SEQUENCE FROM N.A.		NCBT TRAYET=4913:	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bos taurus (Bovine).	Adenine nucleotide translocator 2.	01-JUN-2002 (TremBirel, 21, Last annotation update)	O1-TUN-2002 (TIEMBLIED: 21 (FEEED)		Q8SQH5 PRELIMINARY; PRT; 298 AA.	JLT 1 2H5

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Best Loc
Matches
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J. BIOCHEM. 335:541-547(1998).
INEE MEMBRANE LOCATION: INTEGRAL MEMBRANE PROTEIN
INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIE
EMBL; AB009386; BAA23777.1; -.
R InterPro; IPR001993; Mitoch_Carrier.
R InterPro; IPR002067; Mit_Carrier.
R Pfam; PF00153; mito_carr; 3.
R Pfam; PF00153; mitoch_Carr; 3.
R PRINTS; PR00226; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Trans
SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC
       01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                    Q919M9;
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O46373;
O1-JUN-1998
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TISSUE-SKELETAL MUSCLE;
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ae; Oryctolagus.
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78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 298;
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Query Match
Best Local (
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EMBL; AF231347; AAF63471.1; -
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; MITOCARRIER.
PRINTS; PR000265; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                       Mus musculus (Mouse, Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          Q62164
Q62164;
Laplace C., Costet P
Submitted (SEP-1993)
[2]
                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;

"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and State of Expression During Development.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDR INNER MEMBRANE (BY SIMILARITY).
                                        STRAIN-BALB/C; TIS
Laplace C., Costet
                                                                                                                                                                                                            SLC25A4 OR MANC1 OR ANT1.
                                                                                   SEQUENCE
                                                                                                                        NCBI_TaxID=10090;
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Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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etazoa; Chordata;
theria; Rodentia;
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                                                            N.A.; TISSUE-MUSCLE;
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                     EMBL/GenBank/DDBJ
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Pred. No. 2.1e
L4; Mismatches
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Sciurognathi; Muridae;
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ROTEIN. MITOCHONDRIAL
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InterPro; IPR002067; Mit_carrier.
Pfam; PP00153; Mito_carr; 3.
PRINTS; PR0926; MITOCARRIER.
PROSTITE; PS00215; MITOCH_CARRIER; 3.
Hypothetical protein; Inner membrane;
Transport; Mitochondrion.
SEQUENCE 298 AA; 32904 MW; 3A849FE
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01-MAY-2000 (TrEMBLrel. 20, Las:
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ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Champhibia; Batrachia; Anura; Neol
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MEDLINE-99033429; PubMed-9866197;
MEDLINE-99083429; PubMed-9866197;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic
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L Mol. Biol. Evol. 15:1612-1619(1998).

C -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C -:- SINILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER REMBL; AB008463; BAA36513.1; --

R EMBL; AB008464; BAA36513.1; --

R EMBL; AB008466; BAA36511.1; --

R EMBL; AB008467; BAA36511.1; --

R EMBL; AB008468; BAA36511.1; --

R InterPro; IPR001993; Mitoch_carrier.

R InterPro; IPR002030; Mit_canrier.

R InterPro; IPR002030; Mit_uncoupling.

R Pfam; PF00153; mito_carriar.

R PFINTS; PR00784; MTUNCOUPLING.

R PROSTTE; PS00781; MITOCARRIER.

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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                            Miura I., Ohtani I., Nakamura M., Ichikawa Y., Saitoh K.;
Miura I., Ohtani I., Nakamura M., Ichikawa Y., Saitoh K.;
"The origin and differentiation of the heteromorphic sex chromosomes Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences c a sex-linked gene, ADP/ATP translocase.";
MOL Biol. Evol. 15:1612-1619(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AB008457; BAA36507.1; -.
InterPro; IPR002037; Mitoch carrier.
InterPro; IPR002037; Mitoch carrier.
InterPro; IPR002037; Mitcarrier.
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Ti
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06
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Pred. No. 4.4e-115;
0; Mismatches 15;
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InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of rubripes.";
Submitted (JUL-2001) to EMBL; AF401758; AAL02100
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Eukaryota; Metazoa; Ar
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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NCBI_TaxID=62613;
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                                                                      QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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81.5%;
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Pred. No. 8.5e-106;
6; Mismatches 29;
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095S30
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01-DEC-2001 (TrEMBLrel. 1
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GM12886p (LP02726p).
SESB OR CG16944.
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"Differential regulation of the mitochondrial ADP/ATP in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
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                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Amphibia; Batrachia; Anura; N
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Rana sylvatica (wood frog).
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01-MAR-2002 (TrEMBLrel.
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Neobatrachia;
                                                                                                                                                                                Created)
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a; Ranoidea;
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Ranidae; Rana
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                                                                                                                           SEQUENCE FROM N.A.

STRAIN-SS MAL SEEKING;

STRAIN-SS MAL SEEKING;

STRAIN-SS MAL SEEKING;

"A Chone encoding the ADP/ATP translocase of Lucili
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MIT
                                                                                                                                                                                                                                                                                                                                                              ADP/ATP translocase.
Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
Oestroidea; Calliphoridae; Lucilia.
NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                     -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL EMBL; AF218587; AAF32322.1; -.
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                                                                                                       INNER MEMBRANE (BY SIMILARITY)
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Last sequence up
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01-JUN-1998;
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7237;
                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER EMBL; AF025798; AAB87883.1; -. EMBL; AF025798; AAB87883.1; -. EMBL; AF025798; AAB87883.1; -. EMBL; AF025798; AAB87883.1; -. EMBL; AF001993; Mitoch_carrier. Interpro; IPR001993; Mito_carrier. Interpro; IPR002067; Mito_carrier. Pfam; PF00153; mito_carrier. Pfam; PF00153; mito_carrier. PF00153; MITOCARRIER. 3.
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Pfam; pF00153; mito_carr; 3.

PRINTS; PR00926; MITOCARRIER.

PROSITE; PS00215; MITOCH_CARRIER; 3.

Inner membrane; Mitochondrion; Transi
                                                                                                                                                                                                                                                                        Zeng L.-W., Comeron J.M., Chen B., Kreitman Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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                                                                                                                                   SEQUENCE
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Local Similarity
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                                                  AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA
                 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
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                                                                                      230;
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                                                                                                                                   288
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(TrEMBLrel. 06, Last sequence up
(TrEMBLrel. 20, Last annotation
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                                                                                    Conservative
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31725 MW;
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                                                                                              77.0%;
80.7%;
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                                                                                  Score 1187.5; DB 5;
Pred. No. 5.8e-96;
9; Mismatches 33;
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4; Mismatches
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5459DF0EA0E2E742
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EMBL; AF025799; AABB7884 1; -.
FlyBase; FBgn0023237; Dsub\sesB.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER: 3.
Inner membrane; Mitochondrion; Repeat; Transmem
                                                                                                                                                                                                                                                                                           PRINTER PROSITE; PSOUZI, TOO Inner membrane; Mitoc NON TER 288 28 AA;
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Genetica 0:0-0(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O44094;
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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           KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV
                                              IIYRAAYEGYYDTAKGMLPDFKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGR
                                                                                                             ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI
                                                                                                                                                                                                                AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE
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 KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
                                                                                                                                                              QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
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                                                                                                                                                  QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
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                                                                                                                                                                                                                                                                 Similarity
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muso
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                     Conservative
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31775 MW;
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80.4%;
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06, Last sequence update)
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Pred. No. 1.3e-95;
0; Mismatches 33;
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025129;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-MAR-2002 (TrEMBLrel. C
                                                                                                            062526 PRELIMINARY:
062526:
01-AUG-1998 (TrEMBLrel. (
01-AUG-1998 (TrEMBLrel. (
01-JUN-2001 (TrEMBLrel. )
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER;
PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 304 AA; 33307 MW; 51FD0D7D6B654880 CRC64;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                       ANT2 protein.
ANT2 OR CG1683.
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Eukaryota; Metazoa; Chordata; Uro
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                           PRELIMINARY;
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ne for major mitochondrial
embryogenesis in the asci
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75.88;
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                                                                                                                 . 07, Created)
. 07, Last sequ
. 17, Last anno
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наlocynthia.
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                                                                                                                                                                                                           PRT;
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                                                                                                               sequence update)
annotation update)
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the ascidian Halocynthia
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  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARRIER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Manatil J.F., Asbayani A., An H.-J., Addrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., An H.-J., Addrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ballow R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Despilos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Helman T.J., Mei M.-H., Ilang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mentulov G., Stapleton K.A., Nixon K., Nusskern D.R., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Sher 
                                                                                                                                                                                                                  Query Match
Best Local S
Matches 217
                                                                                                                                                                                                                                                                                           Submitted (MAY-1998) to the EMBL/GenBank/DDBJ database EMBL; AE003484; AAF47956.1; -. EMBL; AE003484; AAF47956.1; -. FlyBase; FBgn0025111; Ant2. InterPro; IPR001993; Mitoch_carrier. InterPro; IPR002067; Mit_carrier. InterPro; IPR002067; Mit_carrier. Pfam; PF00153; mito_carrier. Pfam; PF00153; mito_carrier. 9RINTS; PR00926; MITOCH_CARRIER; UNKNOWN_2. SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061COC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OREGON-R;
                      127
                                                                                                                                        17
                                                             77
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                                                                                                                                                           SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQG
SLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIII
                                                         SFLMDFMMGGVSAAIAKTAVAPIERVKLILQVQEVSKQIAADQRYKGIVDCFIRIPKEQG
                                                                                                                                                                                                                    al Similarity
217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davis A.W.,
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                73.7%; Score 1137.5;
74.8%; Pred. No. 1.56
tive 26; Mismatches
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the EMBL/GenBank/DDBJ
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1.5e-91;
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